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Maximum DB seq length: 2000000000
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                      US-09-938-842A-3729
1677
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10782.626 Million cell updates/sec
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em_htg_hum:*
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Pred. No. is the number of results predicted by chance to have

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

RESULT 1 AX509034 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE	00 4444 2444 2440	0 0 0 40 41	ພພພ	աաաա	0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	0 222 221 221 20 20		c c 112	C 10 8 7 0	ถ ถ	Result No.
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near PAT 27-SEP-20 rophyta; Tracheophyta; core endicots; e; Arabidopsis.	Continuation (12 o AX344558 Sequence AF140509 Apis cera	1595 Homo s 1569 Sequer 5123 Sequer	5986 Dictyos 3092 Naegler 3308 Bombyx	1726 Danio r inuation (22 inuation (3 5920 Dictyos	95302 T7 end 2902 Drosoph 9356 Plasmod	A104010/ BOHUDYA HO ABO70263 Bombyx ma AX599046 Sequence AC117076 Dictyoste U28974 Spiroplasma A1999344 Plasmadin	5577 Dictyos 3339 Bombyx 9768 Bombyx 0264 Bombyx	7738 Eimeria 1261 Danio re 3522 Wigglesw 3364 Human DN	4823 Plasmo 7081 Dictyo 1144 Sequer	9580 Danio r 9580 Danio r 76 Myrmecia 4952 Lotus j	3680 Arabidop 3584 Arabidop 6214 Arabidop 3744 Sequence	scription

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Patent: WO 0216655.A 3729 28-FEB-2002;
The Scripps Research Institute (US) ; {
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77; Conservative 0;
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GCTTTTAACAACTCTCGTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTTA	ATCTCCTTGGACGTGTA	CGTTGAATACTATTCTCACTTGTTTTCCTGCTCCTATATATA	TCGGAATGGTTCTTTAAAGCTCATCGAACATCAGGACCGTTGATTTTTCCCGCATCAA	ATPATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGG	AAAAGAAAAACATTTTGTGAAAAAGAGAAATAAA 	TICTGATTITGGATTTIGAAGCITTTCTTAGGTTAAAAAACAAGTATATTACTA	ABAGCTAGGTATTTCATTTGGGAGTGTACTAGTAACTAGTACTAACCAGAATGA	TTTCCAACCATAGAAAA                 TTTCCAACCATAGAAAA	GGCTTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTT	GCTTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGTA.	GGACGATAGGAGATTTTGGAATCCTTGGAAAGAGGATTATTCCATAGA 	CAAGTACACAAGTACATAAGTATGCGTATATGTATGTGACCGGTTTAATC	
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16 16	CTTTCCCATTGTATCC	TATATCCTGACGAGTC	ATTITICCCGCATCAA	TGTTCACGTGGTACAA              TGTTCACGTGGTACAA	CCCATTGTACAGATGG	TATATTACTAAACAAT	ATGAG ATGAG	ATGGAAATTTTTGTAC                ATGGAAATTTTTGTAC	CTAACCAATAAAAATT                 CTAACCAATAAAAATT	TCCAACCCCAAGTATG	TATTCCATAGACACTA	TGTGACCGGTTTAATC	
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AC003680 91854 bp DNA linear PLN 11-MAR-2002 Arabidopsis thaliana chromosome 2 BAC F17K2 genomic sequence, complete sequence. AC003680 GI:20197048

Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledona; core eudicots;
Spermatophyta; Magnollophyta; eudicotyledona; core eudicots;
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1 (bases 1 to 91854)
Lin, X., Kaul, S., Town, C.D., Benito, M.-I., Creasy, T.H., Haas, B.J.,
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Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.

us-09-938-842a-3729.rge

OMMENT

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/product="expressed protein"
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/gene="At2g45500"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                chouse were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GilmmerA (a variant of GlimmerM, see Mihaela Pertea, http://www.igir.org/schilab/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with BST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypotherical proteins. Genes encoding tRNAs are predicted by KRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/ENAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, http://ttp.genome.washington.edu/RM/Repeatmasker.html).
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KHMIRGMKKKHPVDTTNSHRNAGFSPLTVETAVRSVVPCKDGDDQKHSVSVWGITLPR
VSDEKSTSSCSTDTTITDTALRGEDDDESYLSLFSPGV"
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join(57. 242,335. 747)
gene="At2g45480"
fnote="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="overlap with BAC clone F4L23 (AC002387:1. .1281)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="gynonym: F17K2.2; contains a protein kinase domain
profile (PDOC00100)"
                                                                                                                                                          Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 91854)
Town, C.D. and Kaul, S.
                                                                                                                                                                                                                                                                                                                                                                                                               9712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BAC clone F17K2 is from Arabidopsis thaliana chromosome 2 and is near the molecular marker(s) FLS. The orientation of the sequence is from SP6 to T7 end of the BAC
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                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (27-FPB-2002) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced gi:6598396.
Address all correspondence to:at@tigr.org
            Arabidopsis thaliana chromosome 2 BAC F17K2 genomic sequence
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/mol type="genomic DNA"
/cultivar="Columbia"
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oin(<57. .242,335. .>747)
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/clone="F17K2"
                                                                                           (bases 1 to 91854)
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                                                                                                                                                                                                                                           / Godon start=1
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VAFSILIGGLMLDVLISITLGVSALPVNIIIGVIVVLGLGTALRLTLERCYSWSLRRA
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         /tränslation="MGGKGKKRREKNYLAAHGGPARLPPPPBRSKQDDVpSTLRILMN
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ELAEIDGRSKRKBRSKKYWBAKKQKKNKGKTBDTLRENFPKHGOIRFGVVQAPLKLA
VVPKARKSTLSASQERLRLQAIDAYRSKGWTARPGVPIPAYMAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                        /mote="synonym: F17K2.7"

complement(join(<10833. 11272,11438. 11560,11636. 11237)

12454. 12937,13023. 13119,12524. 13374,12464. 13568,

13645. 12794,13957. 14073,14178. 14264,44350. 14418,

14520. 14576,14730. 14813,14926. 14995,15396. 15538,

15768. 16244,16322. 14665,1655, 17093,17237, 17431,

17612. 1766,18015. 18613,18944. 19249,16533, 17931,1733.
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                                                                                                                                  9822. 10798
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/Aote="st2g45530"
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Ceres:35578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC
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Pred. No. 0;
; Mismatches
                                                  9408. 9427
/rpt family="(CA)"
complement(9578. 9632)
/rpt_family="(GA)n"
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complement(10833. .25573)
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'gene="At2g45530"
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Best Local Similarity 100.0%;
Matches 1677; Conservative 0
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76269 76209 76149 76089 76029 75969 75909 75429 75789 75729 75368 TCGGAATGGTTCTTTAAAGCTCATCGAACAACAGACCGTTGATTTTTCCCGCATCAA 75309 75549 75489 600 1020 1080 1140 1260 1320 1380 099 780 1440 1441 TCGGAATGGTTCTTTAAAGCTCATCGAACACATCAGGACCGTTGATTTTTCCCGCATCAA 1500 540 960 720 840 900 CCTCTGTGGTGGACCCGAATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTT GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTAGCCCTCAACAATGTGTGGAACTGAAG GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTTAGCCCTCCAACAATGTGTGGAACTGAAG TGCTTACGGTCCCTCTTTCTGGTCGTCGTATGTACAAGTAGCATAGCTAGTGGTTCAAA CCCGGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATTAAGTTACGTCG AAGCCTAAAAAGGTTACTACCGGTTTGACCGGTTTATATTTGGTGTTTAATTCTCCC GGATCCGTTTGTTTGTTAATCTCAAGGCCACGTTATCGGCCAATATTTTGATTTTTGAGTG GGATCCGTTTGTTTGTTAGTCTCAAGGCCACGTTATCGCCAATATTTTGATTTTTAAGTG CCCGAAACAAGTACCAACGAATCAAATAAGTTTGAATCGGTTACATCTAGTTACCGTCG AAAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTA TGCTTACGGTCCCTCTTTCTGGTCGGTCGTATGTACAAGTAGCATAGCTAGTGGTTCAAA AACTTACAATCATTTCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATAT 75968 AACTTACAATCATTTCGATTACTTTGATTTCTAGTTCGGTTTGTATTAATAT CCGGATTGTACAAGTACAAGTACATAAGTATGCGTATATGTGTGACCGGTTTAATC TTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGTATG 75788 ATTAGCTTTTTTGGGGGGGGGGGCTTGTGGGCTACATTAATGGGGTCCAAGCTCAAGTATG 75668 ATTGRAAATCTTTCCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTGTAC **AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTGTTTAATTTCTAATCCC** 1081 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATT 75728 GGCTTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATT 1141 ATTGAAAATCTTTCCAACCATAGAAAAGTTAAAATTTGATCAGCGATGGAAATTTTTGTAC AAAGCTAGGTATTTCATTTGGGAGTGTACTAGTAACTAGTAGTACTAACCAGAATGAGT 75548 TICTGATTTTGGATTTTGAAGCTTTTCTTAGGTTTAAAAAAAGAGTATATTACTAAACAAT 1321 AAAAGAAAAACTTTTGFGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGG 75488 AAAAGAAAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGG 1381 TCCCATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAA 75428 TCCCATAATAATACTGATAGAAGATAGGAAAGGTGATGTTTCATGTTCA CGTGGTACAA **AGAGTAGGGTCCAGCTCAGGCCCCACATTCACATTTTCGTTTTGTAGCCTTTCT** 

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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1660)

S Yamda, K., Liu, S.K., Sakano, H., Pham, P. K., Banh, J., Chung, M. K.,

Goldsmith, A.D., Lee, J. M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Goldsmith, A.D., Lee, J. M., Quach, H.L., Toriumi, M., Yu, G., Bowser, L.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T.,

Bavis, R. M., Boker, J. R. and Theologis, A., Shinozaki, K.,

Arabidopsis Pull Length cDNA Clones

L. Unpublished
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S' Yamada,K., Banh,J., Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M.,
Onodera,C.S., Quach,H.L., Tang,C.C., Toriumi,M., Yamanura,Y.,
Yu,G., Yu,S., Bowser,L., Carninci,P., Chen,H., Cheuk,R.,
Hayashizaki,Y., Ishida,J., Jones,T., Kamiya,A., Karlin-Neumann,G.,
Kawai,J., Kim,C., Kosema,E., Lam,B., Lin,J., Meyers,M.C.,
Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T.,
Satou,M., Seki,M., Shinn,P., Southwick,A., Tracy,S.E.,
Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
Direct Submission
Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan
Street, Albany, CA 94710, USA
RIKEN Genomic Sciences Center (GSC) members carried out the
collection and clustering of RAFL CDNA : 'RIKEN
Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J.,
Lucch,M., Kamya,A., Sakurai,T., Carninci,P., Kawai,J.,
Lucch, Luck, Luck
              1286 TTTTTTAGATCATCAAAGGCTCCTACAGATTTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 1345
                                                                                                                                                                                                                                                                                       1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AY056214 1660 bp mRNA linear PLN 18-SEP-2002 Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680)
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Location/Qualifiers
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                                                                                                                      1346 GABATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACAGAGAGA
                                                                                                                                                                                                                                                          1406 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAAGAT
                                                                                                                                                                                                            181 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT
                                                                              121 GAAATTGTGTTTTATTGCAACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA
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Hayashizaki, Y. and Shinozaki, K.
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75308 AAAGCGTIGAATACTATTCTCACTIGITTTCCTGCTCCTATATATATATCTGACGAGTC 75249
                                                                                                                  1561 ACATTTAGTAATCTCCTTGGACGTGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCC 1620
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Arabidopsis thaliana shrunken seed protein (SSE1) mRNA, complete
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AFLOTFTINEHIIBNAPTFRGHVGSSGNDFSLSYPLLIAIIKDLETVVEVAAEHFYG
KKWYNIITETAMKAVIRLAFRNSGYKMILOGETPNEEKORNOSESGNRAGNSGRN
LGPHGLGNONHHNPWYLLGRAMSALSFGRARTTSSTPGWSRIGHQOAVIEPPMI
KERRRTWSELLIFEKGVNGALFAIGEVLYITRPLIYVLFIRKYGWRSWIPMAISLSVDI
LGMGLLANSKWWGEKCKQVHFSGPEKDELRRRKLIWALYLFRYTKYTRQXLESSG
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Lin, Y., Sun, L., Nguyen, L.V., Rachubinski, R.A. and Goodman, H.M. Arabidopsis seeds
Science 284 (5412), 328-330 (1999)
                                                                                                                                                                                                                                        1621 GCTITIAACAACTCTCGTCGTCACCCGTCCGTTTTCTCTCAGCTATTTA 1677
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Lin.Y., Sun,L., Nguyen,L.V. and Goodman,H.M.
Direct Submission
Submitted (19-AUG-1998) Molecular Biology, Massachusetts General
Hospital, 50 Blossom Street, Boston, MA 02114, USA
Location/Qualifiers
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22. .1225
gene="SSB1"
function="required for seed maturation"
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mol_type="mRNA"
cultivar="C24"
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protein_id="AAD30661.1"
db_xref="G1:4837733"
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Best Local Similarity 99.6%; Pred. No. 3.3e-40;
Matches 243; Conservative 0; Mismatches 1
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Mus musculus chromosome 16 clone RP23-1J12, WORKING DRAFT SEQUENCE, ACCEPT OF ACCEPT SEQUENCE, ACCEPT OF ACCEPT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1572 TCTCCTTGGACGTGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAA 1631
                                                                                                                                                                                                                                                                    522 WWRHWINNITDTRYYWWWKRWARBITTVYDSMCNAKGMWRGMNWRAMKOMWAANNDAGAM 463
                                           1002 TINNAMWYATTERMAAYAAAKWAENNAMRWYGAAAGUKWGCWAAMATMGBWWADTAGKWC 943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        282 NNNNKAWYYRIKIVAWCNNRYYYDIAVWIBKRNYKYCYAYBWYYBMYMGKHHWBWWRRAB 223
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Sciurognathi, Muridae, Murinae, Mus.
                         TCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATATCCCGGATTGTACAAG
                                                                                              975 AGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTAATTAGCTTTTTGGT
                                                                                                                                                                                           TITCATITGGGAGIGIACIAGIAACIAGIAAGIACIAACCAGAAIGAGIITICIGATITIG
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Mammalla; Eutheria; Rodentia;
1 (bases 1 to 300695)
DOE Joint Genome Institute.
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AC079431.1 GI:9958043
HTG; HTGS PHASB1; HTGS DRAFT.
Mus musculus (house mouse)
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                                                                                                                                                                                                                                                                                              /product="putative PCF2 DNA binding protein"
/protein.id="AALDOS1."
db xxef="G1:15110351."
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TRELGHKSDGETIRWLLENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTTNADSDMGE
NLMKKKRKRPSNSEYIDISDAVSASSGLAPIATTTTIQPPQALASSTVAQQLLPPQGMY
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PPLQVVPSSGFYSVSDVSGSNISRATSVWAPSSSSGVTTGSSSSI ATTTHTLRDFSL
ETEKQELHQFMSTTTARSSNH"
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/mol type="genomic DNA"
/d_raref="taxon:32630"
/ l. 1141
/note="consensus sequence of A.t., L.a.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               832 others
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Patent: WO 0111061-A 22 15-FEB-2001;
UNIVERSITY OF BRITISH COLUMBIA (CA)
                                                                       /clone="RAFL07-08-P04 (R10678)"
note="This clone is in a modified
(FLC-1) as a BamHI/XhoI insert.
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3.6%; Score 59.8; DB 6;
Best Local Similarity 10.5%; Pred. No. 0.031;
Matches 85; Conservative 299; Mismatches 422;
   thaliana'
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Sequence 22 from Patent W00111061.
AX083744
organism="Arabidopsis
                                                                                                                                                                                                                                        gene="At2g45680"
codon_start=1
evidence=experimental
                 mol_type="mRNA"

db_xref="taxon:3702"

chromosome="2"
                                                                                                                              ecotype: Columbia"
1. .1660
/gene="At2g45680"
1. .102
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/gene="At2g45680"
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Consensus quality: 197223 bases at least Q30
Consensus quality: 197223 bases at least Q30
Consensus quality: 197223 bases at least Q30
Consensus quality: 214345 bases at least Q30
Estimated insert size: 257300; agarose-fp estimation
Quality coverage: 293095; sum-of-contigs estimation
Quality coverage: 3.01 in Q20 bases; agarose-fp estimation
Quality coverage: 2.65 in Q20 bases; agarose-fp estimation
* NOTE: This is a "working draft' sequence. It currently
* consists of 77 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                      2 (Asses 1 to 300695)
DOB Joint Genome Institute.
Direct Submission
Submitted (01-280-2000) Production Sequencing Facility, DOB Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA -----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
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Center clone name: RPCI-23_1J12
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1332 ATTTTGTGAAAAGGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCATAATAA 1391
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                                                                                                                                                                      OK 73019- USA
3 (bases) to 94348)
Kupfer, D. So.S., Wang, H. and Roe; B.A.
Birzet Submission
Direct Submission
Submitted (01-NOV-2002) Department Of Chemistry And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                        Kupfer, D., So.S., Wang, H. and Roe, B.A.
Direct Submission
Submitted (06-NOV-2002) Department Of Chemistry And Biochemistry,
The University of Oklahoma, 620 Parxington Oval, Room 208, Norman,
Ox 22019 HEA
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Submitted (19-NOV-2002) Department Of Chemistry, And Biochemistry,
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
OK 73019, USA
On Nov 6, 2002 this sequence version replaced gi:24462347.
                                                                                                                                          Submitted (05-FEB-2002) Department Of Chemistry And Biochemistry, The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1272 GATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAAACAATAAAAGAAAAC
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Actinopterygii, Neopterygii, Teleostei, Ostariophysi;
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The University Of Oklahoma
Center code: UOKNOR
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/clone="bbusm1:183j13"
/clone=lib="Zebrafish PAc library"
11974 c 1653 g 9348 t
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                                           Kupfer, D., So.S., Wang, H. and Roe, B.A.
Danic rerio PAC Clone busml-183j13
Unpublished
                                                                                               2 [bases 1 to 94348) Kupfer, D.; So, S.; Wang, H. and Roe, B.A. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                             OK 73019; USA.
5 (bases 1 to 94348)
Kupfer, So,S.; Wang,H. and Roe,B.A.
Direct Submission
               riniformes, Cyprinidae; Danio
(bases 1 to 94348)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Danio rerio"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /mol_type="genomic DNA
/strain="AB"
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Matches 160; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA linear VRT 19-NOV-2002 strain AB, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Danio rerio (zebrafish)
Danio rerio
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37747 TATTAATGAAGGNTATTTAATTTAAAATGGGAGTTTAATAAAAAATAAAAAGTAAGAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1313 TAAACAATAAAAGAAAAACATTTTGTGAAAAGAGAAATAAAGTTTA 1358
                                                                                                                                                                                                                                                                                                                                                          f unknown length
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of 10138 bp in length
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unknown length
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unknown length
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of 18480 bp in length
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of 14226 bp in length
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contig of 38029 bp in length
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of 9377 bp in l
unknown length
of 9975 bp in l
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gap of unknown l
                                                                                 4005
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                                                                                                                                                                                  5390
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1. .300695
/organism="Mus musculus"
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Danio rerio clone busm1-183j13 e
AC109580
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87255:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (26-MRR-2002) Yasukazu Nakamura, Kazusa DNA Research
Institute Department of Plant Gene Research; 1532-3, Yana,
Kisarazu, Chiba 292-0812, Japan (E-mail:yn@kazusa.or.jp,
URL:http://www.kazusa.or.jp, Tel:81-438-52-3935,
Fax:81-438-52-3934)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lotus japonicus
Lotus japonicus
Eukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheoph)
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
                                      1332 ATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCATAATAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1055 ATTAATGGGGTCCAACCCCAAGTATGGGCTTACAGCTTTTTCCATAAATTAAAGTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lotus japonicus"
/mol type="genomic DNA"
/db_xref="taxon:34305"
/chromosome="1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="LjT_library"
/note="TAC clone:TM0125"
17797 c 17022 g 27069
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1. .89551
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2 (bases 1 to 89551)
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                                                                                                                                               MPUIS676 1058 bp DNA linear INV 09-FBB-1996 Myrmecia pilosula HI87-128 mitochondrion cytochrome b gene, partial
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LILMTPYLFSDPDNFLPANPLVTPIHIQPEMYFLFAYSILRSIPNKLGGVIALFSSIC
ILYFLPMLNSNMNSSTFYPLSQLLIMLFFMTFMILTWLGSQVIEHPYIIMAQFFSMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mitochondrial-DNA sequence evidence on the phylogeny of Australian jack-jumper ants of the Myrmecia pilosula complex Mol. Phylogenet. Evol. 4 (1), 20-30 (1995) 95346030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           translation="FWGATVITNLVSTIPFLGSDITQWLWGGYSVSNATLSRFYSIHF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITICCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATGAAAATCT 1151
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                                                                                                                                                                                                                                                                                                                                                 Myrmecia pilosuia

Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygot
Neoptera, Endopterygota, Hymenoptera, Apocrita, Aculeata,
Cornicidae, Myrmeciinae, Myrmeciini, Myrmecia,
(bases 1 to 1058)

Crozier, R.H., Dobric, N., Imai, H.T., Graur, D., Cornuet, J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                 mitochondrion Myrmecia pilosula (Australian jumper ant)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2 (bases 1 to 1058)
Crozier, R.H.
Direct Submission
Submitted (08-0CT-1994) Ross H. Crozier, School of Ge Trobe University, Bundoora, Victoria 3083, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                db_xref="taxon:13618"
f'issue_type="head and thorax muscle"
dev_stage="adult worker"
22. .733
88200 TATTATTTAAAATGCAATAAATTAAATTTA 88233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Myrmecia pilosula"
Organelle="mittochondrion"
mol_type="genomic DNA"
strain="H187-128"
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/product="cytochrome b"
/protein_id="AAA86970.1"
/db_xref="GI:576755"
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U15676.1 GI:576754
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                                                                                     RESULT 8
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125556 TTTTTGGAAGAGATATTTCTAATATTTGAAAGATGGCGCCAAAAGTCAATTCTGGCTTTA 125615
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank draft data.html).

NOTE: This is a 'wow.ing draft' sequence. It currently consists of 10 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
                                                                                                             Consensus quality: 148444 bases at least Q40
Consensus quality: 149298 bases at least Q30
Consensus quality: 149814 bases at least Q30
Estimated insert size: 147256; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequencing vector: Plasmid;
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye: 100% of reads
Assembly program: Phrap; version 0.990329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Months of 2199 bp in length to gap of unknown length less contig of 4325 bp in length is contig of 4325 bp in length is gap of unknown length length of 4325 bp in length is gap of unknown length is contig of 13738 bp in length is gap of unknown length is contig of 14787 bp in length is contig of 14787 bp in length is gap of unknown length is contig of 47787 bp in length is gap of unknown length is gap of unknown length is gap of unknown length is contig of 54896 bp in length is gap of unknown length.
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45.8%; Pred. No. 0.35;
tive 0; Mismatches 218; Indels
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gap of unknown length
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47501 a 27383 c 27767 g 47591 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Center clone name: CH224-58F11
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/db_xref="taxon:7460"
                                                            Worley, K.C.
Direct Submission
Submitted (19-MAR-2003) Human
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                                      1 to 151143)
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9405:
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Best Local Similarity 45.8
Matches 184; Conservative
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Muzny, D.M., Adams, C., Adio-Odnola, B., Ali-Osman, F.R., Allen, C., Alabbrooks, S.L., Amazatunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbbrooks, S.L., Amazatunge, H.C., Are, J.R., Ayele, M., Banks, T., Balbbrooks, S.L., Amazatunge, H.C., Burnell, K.L., Byrd, N.C., Burch, P., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T.F., Cater, M., Cavazoes, S.R., Chacko, J., Chavez, D., Cord, C., Coyle, M.D., Dathorne, S.R., David, R., Dayas, C., Coyle, M.D., Dathorne, S.R., David, R., Deladaroy, K.R., Deladaro, C.D., Cox, C., Coyle, M.D., Dathorne, S.R., David, R., Deladaro, C., Edwards, C.C., Blain, G., Durbin, H.H., Delaney, K.R., Delagaro, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Garria, A., Garria, A., Garria, M., Martinez, B., Jang, M., Morris, S., Man, M., M., Martinez, B., Massey, E., Mawhiney, E., Mitch, M., Martina, R., Martina, R., Massey, E., Mawhiney, E., Mitch, M., Martina, R., Martina, R., Massey, E., Mawhiney, R., Martina, R., Martina, R., Massey, R., Martina, R., Martina, R., Massey, R., Martina, M., Martina, M., Martina, M., Martina, M., Marti
                                                                                             TITRACATTITITAAATTIAAGTAGACTGTGAAATAAGCTTAAAAAGGAATAATCTCTA 73324
                                                                                                                                                                                                                       73264
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                                   TITACTGGACCCCATTGTACAGATGGTCCCATAATAATACTGATAGAAGATAGAAGAATG 1414
                                                                                                                                                          1415 GAAAGTGATTTGTTCACGTGGTACAATCGGAATGGTTCTTTAAAGCTCATCGAACACATC 1474
                                                                                                                                                                                                                                                                             1475 AGGACCGTTGATTTTCCCGCATCAAAAGCGTTGAATACTATTCTCACTTGTTTTCCTG 1534
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AC141740.1 HTGS PRAFT.
Apis mellifera (honeybee)
Apis mellifera (honeybee)
Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Aposidea;
                                                                                                                                                                                                                   73323 GCTATATGTAGCGTGAAATTTATCACATGGTATGATTAATTCTTATTGTGGAATAATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AC141740 151143 bp DNA linear HTG 19-M2
Apis mellifera clone CH224-58F11, WORKING DRAFT SEQUENCE, 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTTCCTTATAT 73193
                                                                                                                                                                                                                                                                                                                                                                                                    1535 CTCCTATATAT 1545
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125676 AAIGACACTGATTTIAATATTTITAATCIATTITTATCCITTTTTCAITIGITTTAI 125735
                                                                                                                                                                                          125796 GGAAATAATTATCTTAATTTATAATATAAAAATATAGATATAGATAAAAGATACAAATA 125855
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                                                                                                                                               AGGTATTTCATTTGGGAGTGTACTAGTAACTAGTAGTACTAACCAGAATGAGTTTCTGA 1266
                                                1147 AATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCT 1206
                                                                                                                                                                                                                                        1267 TTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGA 1326
                                                                                                                                                                                                                                                                                                                                       1327 AAAACATTTTGTGAAAAAGAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCAT 1386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genome sequence of the human malaria parasite Plasmodium falciparum
Nature 419 (6906), 498-511 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MSKTEYDILSLVNAVEFSKYCSEYKKRHLTNYIQSCSVKNQIN
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DKLNNENI LEDKNKRNI CEHI KSKI NDKNFVQNNDYGKNI KI INNI NEQNLLMKDKND
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Submitted (13-5EP-2002) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum 3D7
Plasmodium falciparum 3D7
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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protein id="AAN37021.1"
db xref="GI:23497479"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    125916 ACAGATAATTAATTAAATGTCATAATGAAATATAATTATTT 125957
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"mol type="genomic DNA"
'isolate="3D7"
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/locus_tag="pp14_0408"
complement (<357. .>4163)
/locus_tag="pp14_0408"
complement (357. .4163)
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chromosome="14"
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AE014823 AE014187
AE014823.1 GI:23497478
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NIMDGKGNILLNINTSDEYGSIGDEYKNIEMULLCQEQNINNTYIQKCAFELNINSTYNNINDGKGNILLNINGHEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEGORYLLINGGEG
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Rlatvrnvonilnkkninktdeneekktlinnnfktntglentkptiinestfnryv
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EHEEGGEDDNDDEYDRONNEOEDHFBDEDYYAENDHNNNNNNNNN INNRSFKFNRSS
KNKYDENDFINHKKAKAKGDEEYEDDEENDDGYDEDGGGSYKYNNNSKDDNTFNKKN
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IDTGIKNNVIECEKHMQLLISPGDMYMFKNQSHEMBARLLLIVCNKONQPFDVKMHIK
DPQMNNEK"
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ILPEPLTKKILPDYQNIYRPIXSIYSYIGPPPYMINNCRIPHIFTKHGLIILKKFTT
DNAYENYIKEEQLNQEDDBEIVFNSNDPPRLNKKONILTKDLLKNKNPNTSTPRKRNN
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QNSLGSILNKTNSFNKNDNNSTQEBIKVKRRRGRPKASEVAAINIMNKLKQNDIRKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNNEI YYDVCYPSDNLLKNNFQISDTLFVDFLSSLLQIDPSKRCNAMEALKHPWLQPN
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1958. 4387
17pt_tvpe=tandem
1543. 4577
17pt_tvpe=candem
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rpt_type≑tandem
186. .4225
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protein id="AAN37022.1"
db xref="GI:23497480"
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/rpt_type=tandem
:352. .5382
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locus tag="PF14 0410"
oin(9317. .9689,9836:
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b_xref="GI:23497481"
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8386...8438
/rpt_type=tandem
9083...9109
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9797.8020
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9317...>11238
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264. .9293
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LQEELLKKI PNVNNKDVSFNIYDTKKDHSLCSBALYDYMDIFKIILNKIQKDKNIHEN
LSVVNSVLILNMLSRINFCNYEIFKFFTKNYYKNLNDKDLEPHHFTLLLNSFAKCNIH
INIMKYILKYMNNKNFINNLSYVNITNAVHYYMAKFNYRNATFLNHLKDKVIEIIDIIP
                                                                                                                                                          QREPSNIMWSLAKLHIKDDYPYYIAFQKIKQIIDVMDWMSVAQILDAMRRKKNYSNGQ
DIGATIKEKKNLENDISCPLRDIKDTTLNGQNIDYKNNIEHNKYHNBERVKEKRIIT
TQTTTQNKDLNNNIQLTYKTPENNIISIEKNINTYNIISDDLEKNILHLLVNKYIKHI
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ICTRIDNIQDIAISDNDKYIYACGENRLIEIFDIYEENRKRCNNDIGKYVDVSIPSII
KNTKLKMKNCSESDNMKHNNILLSKNALDNKYIPYHKTKYKNISNGKSIYIPIYNYED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSICYSSLTFDLSKDKFNNILMTSGYDGYIRLYDISNNIIKSPYDEEKSITHCMFSN
NNKYIISTNKSKFGKVFDFWYMNKMNSKMMATYLMNYKTYCLNKFLIRKENLENENY
HDTINEDDIFSSQLYNDKEYALCKIGNIFEDEELEERIKIVNELNRKINEQENKHFEP
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NSDSSIYDENTIKSNTFYEHVINKLEPTWSLFVDILKKYMDLVPYDNINDSLKKINYNY
KSYFNHINFILNTNYHSLNIDEKEPSLYYMLSEIISNEDDIFKFSSCIAGDKCIIPSID
                                                                                                                                                                                                                                           QHCSLHVLTQVPFCCLQLMYINSDIYYKSLEILRKKRNDMTTLNLIYAKYFLRIFIEK
QEAHFQKLPRSLKQFAKEILNSDNN"
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VLKIWDLRMNLFNISKKSSRSNKSDIIFIDNKNPFASICSHEDTVTSITFNKTIDHEG
SYKLKKEQRKKKKIFNSKKECIDNKNVYSSSIDCENMNDSTSDYEEDRESDNSSVSSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YAHVYDLYTGFHVNSIKNLYLPNYYVDNHSYYSHSIDTNKKRISFLTSVDTYPKNQN
.IATSNGYPDGSIVLWAFVAF"
                       ILKI I EKYNEKNYKDTKILKCSYDVFKNNVHRYSFDQINKI IRLYNI SEIYDIHFNTS
VFNY I I KRLDAI PPYVVVNVFHRLRDYNNINLI KEYFI KNI DKFNNLDLTI ILSSFTI
translation="MRKLLSTAIMDLKKIKGNNFESKHCNDNLKSLIIKNIHKFENDE"
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complement(join(<12999, .15334,15524, .>15647))
/locus_teg="PF14_0412"
complement(join(12999, .15334,15524, .15647))
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product="hypothetical protein"
protein_id="AAN37026.1"
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15809. .15855
Typt_type=tandem
complement(a17033. .>19621)
/locus_tag="PF14_0413"
complement(a17033. .>19621)
/locus_tag="PP14_0413"
complement(17033. .19621)
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complement(<12999.
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/rpt_type=tandem
15450. .15497
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190305 ATATACTCCTGTGCATTATATAAAAATTTATGTTGAATACATAAAATAATATTATTTCTACA 190246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         56956 bp DNA linear HTG 24-MAY-2002
Dictyostellum discoldeum chromosome 2 map 4903137-4960091 strain
AX4, *** SEQUENCING IN PROGRESS ***.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TTGGAATCCTGGAAAGAGGATTATTCCATAGACACTAATTAGCTTTTTGGTGGCGCAGCC 1043
                                                                                                                                                                                                      743
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1 (bases 1 to 56956)
Gloeckner,G., Eichinger,L., Szafranski,K., Pachebat,J., Dear,P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               189945 GACAAAACTATATTATTAATTCATATATTTTGTAAAACCTGTTATAATTAACGATAAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1223 AGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTTGGATTTTTGAAGC
                                                                                                                                                                                                        ACATTCACATTTCGTTTTGTAGCCTTTCTTTTCTGGTGCTTACGGTCCCTCTTTCTGGT
                                                                                                                                                                                                                                                                                CGGTCGTATGTACAAGTAGCATAGCTAGTGGTTCAAACCCGGAAACAAGTACCAACGAATC
                                                                                                                                                                                                                                                                                                                                                         AAAATAAGTTTGAATCGGTTACATCTAGTTACCGTCGAACTTACAATCATTTCGATTACT
                                                                                                                                                                                                                                                                                                                                                                                           TATATATATATATATATATATATATATAAAAAAAATTAAATTTGACCATATTTGATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1044 TTGTGACCTACATTAATGGGGTCCAACCCCAAGTATGGGCTTACAGCTTTTTCCATAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1163 GAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGTATTTCATTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TIGATCIGATITICIAGITICGGITITGIATGITITAATATICCGGATIGIACAAGIACAAGI
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                                                                                                                                                                  Gaps
                                                                                                                             3.2%; Score 53.2; DB 3; Length 249943;
.larity 43.4%; Pred. No. 0.32;
Conservative 0; Mismatches 383; Indels 1;
xref="GI:23497484"
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HTG; HTGS PHASE2.
Dictyostellum discoideum
Dictyostellum discoideum
                                                                                                                                               Similarity
                                                                                                                                                                 294;
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SATWAILDSAAKGKPWTVSYINGVIAGLAGITPSAGYINGVGSTSIGGICLGLASYYSV
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LGVVSVAVWAAAWTWVLLKIIDATIGVKIDESBEELGLDLVEHGEFAYHNISLQGNEN
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QLSKLETTEGHLKYRKIISKWPYKOGPKNIELEGGAFKGIEKGILDISSNNNNNNN
NNNNNNNNNNNNNNNNNNNNNNNNNNNIVELKGGAFKGIEKGILDISSNNNNNNNN
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PNKKINNQVBSIRIDSGPVBFPLQLVYYELTYLHTLEFPHPRIMLLGJGIGKHJKCR
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SRHVKKIFSNGIKQLLSSSTFKYFKFSNWYDIISIDTFSELKNNKTLKKLVYKEKFHY
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NNNNNIVELIVYDFLLENDAEEGFYNLLPKEDDEYGIYKDLQPILYLNTIDYEGSQDD
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QNYELTNLHTLSIPLHFHQMILLQDGIEBEHGRGDLLEHTDNVMQDWDKMIQSLLA
SKSIKNFRIENKCYLGECINQSIKSYNENYSAARQVKKLSBGGRQLLESSTFKYF
YLYNMHDI ISIDTESELKNNKTLKKLYRPLYNYCLANKEBVABHQFNIYL
YESNOASGSGALSMYKHFKFBLEFPPKLKLIFESLFHYNYFQLYSTIVIYELYB
ELLNEIINLSNKISKVQQQQQQSIKEFKIVINKKINNKHFQTILNDRNINGDNG
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GIIGNLDHAFLINVSYDDCSPNAPNIPAAAYAFFWMMPANITPLLMTGAFAERVKFKA
FIALTVAWEIIVFYPVAHWIWGGGWLHKYFGVLDFAGGIVIHTSAGVSALVIALYVGR
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PESLFKHYWYEQLYSTTIVIYDTLYEELLNEIINLSNKISKVQQQQQQQQQSIKEFKI
PIKMYSDNKHFQSILNDRNINGDNGLFVITVSNKKRLC"
complement (join117912 . .18092, 18308 . .18333))
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Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular
Submitted (24-MAY-2002) Genome Analysis, Institute of Molecular
Biotechnology, Beutenberstr. 11, Jena 07745, Germany
CDS predictions from GeneID may contain errors. Further Information
is available from IMB Jena, Department of Genome Analysis
(http://genome.imb-jena.de/dictyostelium/)
intip://www.uni-koeln.de/dictyostelium/project.shtml
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YCLSDIGKCKCDPTHQGGDCSLPYIECLMDCMNVGQCNNQTGICSCPISPYEMSGIDC
SIPLHTISAVSPSDTNGGSASIYGMFSNNHTYLQVFIGNKQIPIYYIISKSEIICKAP
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STGLKSUSVIGNSINVTSKDIYQYYSUDKQCPHYTTGYTGYTCKAP
OLNEYLLLNKWSIGSDNGGALPGSNTTIDGNTGNTTTNTNYDQTYYQILTTKLIEIDFNGN
QINEYLLLNKWSISBYQSSNLNTLQLQMKSSVNBIQTNTTNDGINKDRTTFAGINFKLT
SGSVKMTYSISBYQSSNLNTLQLQMKSSVNBIQTNDGNBDTFFAGINFKLT
NYYTIKKDAKVLNGRFIDBISGGISTFWQTVLVSKSNDSITVGWNLPHQDNS
DFSVLVSPEFVDECGGDNDRKSWFLPVVIVVBIVFTLIIIFVVITIKKRFVEMYLFR
SKIKQLANLNK"
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KFNNVKGFVQIELIEGYNQTSWSNIKEIGNVTNIYIRTNDLTEFPNDHLSNIRSDSIE
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SKSNPNYTFTLSLGIPPILNLVDWQSSTTDLVIDGSFFTYNSSIINITIGNENCLVTN
       Lehmann, R., Baumgart, C., Parra, G., April, J.F., Guigo, R., Kumpf, K., Tunggal, B., Cox, E., Quail, M.A., Platzer, M., Rosenthal, A. and Noggel, A.A. A. Sequence and Analysis of Chromosome 2 of Dictyostelium Unpublished
                                                                                                                                                                                                                                                                                                             Submitted (06-APR-2002) Genome Analysis, Institute of Molecular Biotechnology, Beutenberstr. 11, Jena 07745, Germany 3 (bases 1 to 56956)
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8472. .8483)
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NOTE: This is a 'working draft' sequence.
This sequence will be replaced
by the finished sequence as soon as it is available and
the accession number will be preserved.
Location/Qualifiers
                                                                                                                                                                                   The Dictyostelium Genome Sequencing Consortium 2 (bases 1 to 56956)

    .56956
/organism="Dictyostelium discoideum"
/mol type="genomic DNA"
/strain="AX4"

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join(3306. 3318, 3871. 4174)
join(3306. 3319. 1000
codon start=1
product="hypothetical protein"
protein id="AAM43758.1"
db_xref="GI:21166141"
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|John(8654 . 89006 . 11010)
|John(8654 . 1010d_02932" |
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/note="ORF_ID:dd_02927"
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join(33. .523,639. .263
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/chromosome="2"
                                                                                                                                                                                                                                                       Baumgart, C.
Direct Submission
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AC004401.3 GI:20197125
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Best Local Similarity 47.1%;
Matches 161; Conservative 0
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KKSEEKROKKI AEAKOSLDNPYSEREAKKKTALKONRDHNKSLETDSTSGNTTHTWES
VSMIDLQAKPNPANKDTSRMREILIRLKNOPIV"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAAÄTC: 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1151 TITCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT 1210
                                                                                                                                 KEAIFSEDOVRFYMAELILALEHLHDSNIVHRDLKFENILLDSQGHCILTDFGLÄKLB.
KYNNETPSRAGTLEYMAPPALQHATOKAVOWASIGILMPDMIGKPPEHKNRALM
OBKIISEKAKPRKPYSSSARSLINGLIKDPFKRLGANGAIETKRHPPFKSLOMKKIE
NKEITPPFVPSTKGIDDISNPDHASLKAHQRDSFSTSPTLSSSQQAYFDGFSFVRTPV
                                                                                                                                                                                                                                                                                  product="hypothetical protein"
protein id="AAM43766.1"
db xref="G1:1166149"
translation="MSDPFGEENVEITEEFVEGDINENDLIDGNVEYVDGNGISPETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rotein id="AAM43767.1"
b_xref="G1:21166150"
ranslation="MKRFISTTSLRVLSNLNKONNNNKFNKSIVGVFNREFSSSNEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNKVNFGENNNSSTTEPTKVLFNDSQFYQEDKYQGISKEPPSKEIVDTLLADLNPDDI
EIKPDGLIYLPPIKXRILNQAFGPGGWALKPPGPPVVEGKTLIRPYALYCLGRYVAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GEQQYVPNSFISFATATESAKSNALVRCCKDLGIGSSLWDPIFIROWKSEYATERW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CENSKTKERRLFWFLSNRSENQLPYPWKESDFNQVPSNSSYSSSSSINNNSNSSNNN
NNNSDSSSSINQPQQETISYHQDDSSSPSSKITEQQDDSEDIDIDDVVPPQLKKYAGK
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                                                                                               DFTPLCNGAQETEIVKISNSINLSNFIIKELVGKGGFGKVFQVVHVDTQKVYALKVIK
CNHILAKKSVVNTLAEKDILKKISHPFIVNLHYAPONEKKLYLVMDFVNGGOLFYHLO
                                                                            KNTIISTSPTECEESSSSTITTPSEESLSSGEESSSISDSESKIITIATLLKPSNSVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                      codon start=1

product="Mitochondrial genome maintenance protein MGM101
                                                                                                                                                                                                                                                                                                                                                                                                                    52746 Triparitaradargegariraiarriadaagrirriarrarararagegeger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         52866 AATGTAACCAAAAAAAAAAAAAAAAAATAGATGTGTGGGGATTAGAAAGAAATAAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT
serine/threonine kinase homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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0
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                                                                                                                                                                                                                          complement (join (24089. .24410,24517. .24779))
/note="ORF ID:dd_02931"
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IWRQLVADPKGLSYLQWASSSFDNAPKIKSQATAILEFINKSQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 52.6; DB 2; Length 5
Pred. No. 0.54;
0; Mismatches 194; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (26482, .27039)
/note="ORF_ID:dd_03240"
/codon_start=1
                    protein id="AAM43765.1"
db xref="GI:21166148"
                                                                                                                                                                                                                                                                                                                                                                                                                                          ID:dd_02934"
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ilarity 46.6%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          note="ORF
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Best Local Similarity
Matches 169; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1451 TCT 1453
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linear PLN 11-MAR-2002
PAT 08-JUL-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1135 AAAATTATTGAAAATCTTTCCAACCATAGAAAGTTAAAATTTGATCAGCGATGGAAATTT 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1019 ATTAGGTTCGTATCTCTTTAACTATAAAAAAAAAAACTATATGAATGGATATGAAATG 960
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliams
Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        839 AAGTGTTTTTTTTTTTTTTTTTTTTAAACACGTTAAAGAACCGAAACTTGATCAGTTATTA 780
                                                                                                                                                                                Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1315 AACAATAAAAGAAAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            779 GACAAGCGAAGCTACCCTTTGTGTTTGTTGACGATCCTATAATAAAGTTTTTCACGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1255 ATGAGTTTCTGATTTTTGGATTTTTGAAGCTTTTTGGTTTAAAAAAACAAGTATTACTA
                                                                                                                                                                                                                                                                                    Budworth, P., Brown, D., Chang, H.S., Zhu, T., Han, B., Wang, X. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 clone F21P24 map CIC06C07
                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches 181; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2000;
                                                                                                                                                                                                                                                                                                                                         gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1375 AGATGGTCCCATAATAATACTGATAGAAGATAGAGCAATGGA 1416
  linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          thaliana"
                                                                                                                                                                                Eukaryota, Viridiplantae, Streptophyta;
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  DNA
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Promoters for regulation of plant ge
Patent: WO 0198480.A 73 27-DEC-2001,
Syngenta Patricipations AG (CH)
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Sequence 73 from Patent W00198480.
                                                                                                                               Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis t
/mol_type="genomic DNA"
/db_xref="taxon:3702"
_371 c 305 g 63
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Arabidopsis thaliana chromosome
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us-09-938-842a-3729.rge

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complement (11836. 11877)
/rpt family="AT rich"
complement (13949. 14008)
/rpt family="(TA)"
complement (15667. 15687)
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17877. :21740
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14407. .14452,1455:
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                                                421. .10087
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        repeat region
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                                             gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="synonym: F21P24.1"
oin(<1. .92,168. .326,400. .571,679. .977,1088: >:>1327)
gene="At2g22950"
                                                                                                                                           Submitted (09-MAR-2000) The Institute for Genomic Research, 9712-Wedical Center Dr., Rockville, MD 20850, USA
3 (Dases I to 94038)
Town, C.D. and Kaul, S.
                                                                                                    VGSDSTLVLNTLIFNCFVPCQVFNEVSSREMEEIDVFKGILDNTVFVVTGGTVFFO,
IIIEFLGTFASTTPLTIVQMFFSIFVGFLGMPIAAGLKKIPV"
omplement (594. .665)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     trānslation="ILTDDGIAIEGPVFREKNOBEMLELIPKIQVMARSSPMDKHĽV
QLRTTFDEVVAVTGDGTNDAPALHEADIGLAMGIAGTEVAKEIADVIILDDNFSTIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TVAKWGRSVYINIQKFVQFQLTVNVVALIVNFSACLTGSAPLTAVQLLMVNKIMDTL
GALALATEPFNNELMKRMPVGRRGNFITNAMWRNILGQAVYQFIIIMILQAKGKSMFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      translation="MRTFSPKLLLLLLLVLRHHAESGSIVKFLPGFEGPLPFELETGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IGIGTLAKYWANDERVREALQIRKGSIGKWIRCNSNIHYDDDIISSIPYHMNÄSINGY
RSLIYSGDHDMEVPFLATBAWIRSLNYPIIDDWRPWIINNQIAGYTMTYANKYTYATI
                                                                                                                                                                                                                          Direct Submitseion
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA, cdtown@tigr.org
On Apr 18, 2002 this sequence version replaced g1:6598413.
Rounsley, S.D., Lin, X., Ketchum, K.A., Crosby, M.L., Brandon, R.C., Sykes, S.M., Kaul, S., Mason, T.M., Kerlavage, A.R., Adams, M.D., Somerville, C.R. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oin(1. .92,168. .326,400. .571,679. .977,1088. .1327).
Gene="At2g22950"
                                                                   .3156,3867. .3985,
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Tocte="synonym: F21P24.2"
1057. .4170,4277. .4326,4417. .>4493)
Gene="At2g22960"
1057. .4170,4277. .4326,4417. .4493)
Gene="At704277. .4326,4417. .4493)
Gene="At704277. .4326,4417. .4493)
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product="putative serine carboxypeptidase 1"
protein_id="APM14928]1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="overlap with BAC clone=T20K9
AC004786:64143. .86686)."
                                                                                                                                                                                                                                                                                                                                             Organism="Arabidopsis thaliana"
mol type="genomic DNA"
cultivar="Colubia"
db_xref="taxon:3702"
chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'codon_start=1
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'db_xref="G1:20197127"
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rpt_family="(TAAAAA)n"
891. 1968
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complement(4633..4653)
/rpt_family="AT_rich"
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/rpt_family="AT_rich"
4553. .4583
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155. .4493
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gene="At2g22960"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene="At2g22950"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             map="CIC06C07"
clone="F21P24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ranslation"
                                                                                  (bases 1 to 94038)
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                                                                                                                            rect Submission
                                                             npublished
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  AUTHORS
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                                                                                  SFERENCE
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/ Octo="synonym: P21P24.3; supported by cDNA:
// Octo="synonym: P21P24.3; supported by cDNA: 7160,
// Octo="startar" o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Jan(10590 ... 10717,10800 ... 10945,11012 ... 11088,11168 ... 11290, 1602 ... 11704,11806 ... 11828,11912 ... 12011,12378 ... 12464, 2552 ... 12620,12727 ... 12798,13609 ... 13730,14190 ... 14303, 4407 ... 14452,14559 ... 14639)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4. 18289,18426 .18502,18632. 18751,
9242,19338. 19439,19871. 19957,
0397,20476. 20594,21039. 21152,
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GSVPSLVSTTYSMTKMANIIFLDOPVGSGFSYSRTPLVDKISDTGEVKRIYEFLÜKKL
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AYHMKNSIDGYRSLIYNGDHDMMYPPLATQAMIRSLNYSITDDWKPWMINDQIAGYTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LSPDCDTASPDCYLYPFYLISFWANDESVRDALHVNKRSIGKWERCNYLSKPYNKDIK
SSVPYHMNNSVSGYRSLIYSGDHDLVVPFLATQAMIKSLNYSIIDEWRPWMIRDQITG
YTRTYSNROYTRATVKGSGHTAENKPQESFIMFRRWINGQPL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GIGEEEEVQLFYYFIKSERNPKEDPILLMLSGGPGCSSITGLLFÇNGPLALKSEVYNG
SYSELVSTYYSWIKTANIITPLDQVVAAGESYRARDLIDTPTGEVKEHTBFLQORLS
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NYRIPFSHGMALISDELYESIREACKGNYFWNDPRNTKCLKLVEEFHKCTDKLNEFHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ranslation="MSLTLEFLLLLIVLILSHMAHSGSIVKFLPGFEGPLPFELETGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       product="putative serine carboxypeptidase I"
protein id="AAC17815.1"
db_xref="GI:3169172"
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1 14334757 gb AY035052 1 "
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LLELFEKQKLKFTFSLSEKI IKKY ILFMHKYNYKKFNLINI I EIRLDNTI FNLGYSIT
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NIYDTI YICKNTLISI IYSILNIYNNNYNNILIMKYYSY "
                                                                                                                                                     Eimeria tenella
Bukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Eimeriidae;
                        circular INV 02-JUN-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MLRYLGPKLKKLKRINIHMQPBFSTKYFILNTNKYNNKMILSFY
                                                                                                                                                                                                            1 (bases 1 to 34750)

Cai,X. and Zhu,G.

Eimeria tenella plastid genome complete sequence
Unpublished
2 (bases 1 to 34750)

Cai,X. and Zhu,G.

Direct Submission
Submitted (13-JAN-2003) Veterinary Pathobiology, Texas A&M
University, 4467 TAMU, College Station, TX 77843-4467, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement (13. .85)

product = rRAN-11e"

/anticodon=(pos:51. 53, aa:11e)

complement (246. .1754)

product = 16S small subunit ribosomal RNA"

/product = 1885)
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1176. 5247
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Eimeria tenella chloroplast, complete genome.
AY217738
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(transT_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                               l. .34750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (2182. . 2253)
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product="tRNA-His"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="tRNA-Leu"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;231. .6307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .323. .6409
'product="tRNA-Tyr"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product="tRNA-Ser"
                                                                                                                                 chloroplast Eimeria tenella
                                                                                      AY217738.1 GI:31322455
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/note="RPS4"
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                        LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
                                                                                                                              SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                               source
                                                                                                                                                                                                              REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
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JOURNAL
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join(17954. .18072,18144. .18289,18426. .18502,18632. .18751,
19006. .19108,19205. .19242,19338. .19439,19871. .19957,
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YTRAYSNKWTFALIKASGHTARYRNETFINFQRWISGQPL"
COMPLEMENT (18316. .18358)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72622 AGAAAATTGAAGTACGAAACAGGTCCTAAAACTGTTCCTATTTTATTTGGTATGATATCAT 72563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             72502 AAGTGTTTTTTTTTTTTTTTTTTTTAAACACGTTAAAGAACCGAAACTTGATCAGTTATTA 72443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72442 GACAAGCGAAGCTACCCTTTGTGTTTGACGATCCTATAAAAGTTTTTCACGGAAC 72383
                                                                                                                                                                                                            GEDENVQFFYYFIKSENNPKEDPLLIMLNGGPGCSCLGGIIFENGPVGLKFEVFNGSA
PSLFSTTYSWTKMANIIFLDQPVGSGFSYSKTPIDKTGDISEVKRTHEFLQKWLSRHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1135 AAAATTATTGAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTT 1194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1075 AGTATGGGCTTACAGCTTTTCCATAAATTAAAGTAAATCTTTTTGCCTAACCAATA 1134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1255 ATGAGTITCTGATTTTTGGAGCTTTTCTTAGGTTAAAAACAAGTATATTACTA 1314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1315 AACAATAAAAGAAAAACATTTTGTGAAAAAGAGAAATAAAGTTTACTGGACCCCATTGTAC 1374
                                                                                                                                                                                          translation="MSLKIKFLLLLVLYHHVDSASIVKFLPGFEGPLPFELETGYIGI"
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eres:33165"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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Pred. No. 0.55;
0; Mismatches 181; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    72382 GCCCTGACGGTĎAŤCGCATCGGĎAGAAGATCCGŮCGA 72341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /rpt family="AT rich"
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                                                                                                                                                                                                                                                                                                                                                                                                                                             .19848
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Best Local Similarity 47.1%;
Matches 161; Conservative
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                                                                                                                                                                                                                                                                                                                                                               repeat_region
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15

RESULT

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                                                                                                                                                                           \(\) \text{tensiation="mtQINTYFNIADNSGVKKILCIQNLTKKTKKIEIGDLIVGVIKK \) \text{INNTSKLIYSNIVYGIVIELKKNINLYKKYNISPNDNSAVLVDKNLNPIGSRIFGTIP \) \text{KFIKKNYLKLYSLIVDFI" \)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YNKYLLENTIEQKILLIKKYSKTRAKGRIKKYKIIIIIGNKEGWFGTOCSKDYYLQDA
ISKARLHAFKNIYIISLFYSNLLKNNIYIKKKFKKLYLFSYNYKIKISSSYIIRLLFY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MKVKLSIKRLCKNGFLINROKRKYIYGVKFLNITTDKNNKNLNI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6842 recectráctica estracio entre recontracio de la recontración de la reconstructor d
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1154 CCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGTATT
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Best Local Similarity
Matches 173; Conserv
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                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                   of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                               2552756 segs, 1349719017 residues
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                                                                                                                                           2004, 21:36:05
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Listing first 45 summaries
                                                                                                M nucleic - nucleic search, using sw model
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses Claim 144; SEQ ID NO 3729; 577pp + Sequence Listing; English

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The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) conteacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloric stress; The present sequence is that of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 1677 BP; 508 A; 292 C; 335 G; 542 T; 0 Other;

Score 1677; DB 24; Length 1677; Pred. No. 0; O; Mismatches 0; Indels 0; Query Match
Best Local Similarity 100.0%;
Matches 1677; Conservative 0 ठ

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120

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> TAATGAATGGTATGCTGATGGTAGGCAAAAGTTGGTGGCTGCGAAAATTACAACATTATC CCTCTGTGGGACCCGAATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTTT 361 421

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1320 1020 1020 1080 1080 1140 1200 1200 1260 1380 1440 1500 1620 960 960 780 840 900 006 GCTTTTAACAACTCTCGTCGTCGTCCCCCCGTCGGTTTTCTCTCAGCTATATTTA 1677 721 TGCTTACGGTCCCTCTTCTGGTCGGTCGTATGTACAAGTAGCATAGCTAGTTGTTCAAA 1021 AFTAGGTTTTTTGGTGGCGCAGCCTTGTGGTATATGGGGTCCAACCCCAAGTATG 1441 TCGCAATGGTTCTTTAAAGCTCATCGAACACATCAGGACCGTTGATTTTTCCCGCCATCAA 781 CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACGTCG 841. AACTIACAATCATITICGATIACTITIGATITICIAGITICGAGITIGIATITITIAATAT 1141 ATTGAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGGGATGGAAATTTTGTAC TICTGATTITGGATTITGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAACAAT TTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAAAAT TCCGTTATTATTACTGATAGAAGATAGAGGAATGGAAAGTGATTTGTTCACGTGGTACAA 781 CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATGGGTTACATCTAGTTACCGTGG 841 AACTTACAATCATTTCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATAT AAAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGGATTATTCCATAGACACA ATTAGCTTTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGTATG 1081 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATT 1141 ATTGAAAATCTTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTAC <u>aaaagaaaaacattttgtgaaaaagagaaataaagtttacttggaccccattgtacagatgg</u> aaaagaaaaacattttgtgaaaaagagaaataaagtttactggaccccattgtacagatgg TCCCATAATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAA TCGGAATGGTTCTTTAAAGCTCATCGAACACATCAGGACCGTTGATTTTCCCGCATCAA AAAGGACGGACGATAGGAGGATTTTGAAATCCTGQAAGAATTATTCATAGACATA GGCTTACAGCTTTTCCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAAATT 961 1021 1081 1201 1201 1261 1381 1381 1501 1501 1561 1621 1621 661 1261 1321 1321 721 196

AAA88782 standard; cDNA; 1483 AAA88782; RESULT 2
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(first entry)

19-FEB-2001

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modifying desiccation tolerance.
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Arabidopsis thaliana SSE1 cDNA
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Best Local Similarity 99.6%;
Matches 243; Conservative C
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                                                                                                                                                                                                          99US-0128651
                                                                                                                                                                                                                                (GEHO ) GEN HOSPITAL CORP.
                                                         Arabidopsis thaliana.
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The present invention describes a method for detecting and differentiating between haematopoietic cell proliferative disorders associated with at least 1 gens and/or their regulatory regions in a subject. The method comprises contacting a target nucleic acid in a biological sample obtained from the subject with at least 1 reagent, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. ABZ09861 to ABZ11118 represent specifically claimed nucleotide sequences from the present invention. Oligonucleotides from the present invention on be used: for invention. Oligonucleotides from the present invention can be used: for discrete haematopoietic cells; for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia; as probes for determining the cytosine methylation state-and/or-single-nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and/or single-nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation of secent invention can subclasses, diagnosis, prognosis, treatment and/or contacting a predisposition to, differentiation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders The present method enables chaematopoietic cell proliferative disorders The present method enables can highly specific classification of haematopoietic-cell proliferative disorders allowing for improved and informed treatment: of patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1091 TITITCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAAATC 1150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG dinucleotides
                                                                                                                                                                      Haematopoietic cell proliferation disorder related DNA sequence #386.
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                                                                                                                                                                                                                   gene therapy; lymphocytic leukaemia; acute myelogenous leukaemia; cytosine methylation state; gene; ds.
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Best Local Similarity 49.4%; Pred. No. 0.088;
Matches 131; Conservative 0; Mismatches 134; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         , Braun A, Distler J, Guetig D, Howe A, Mueller J Piepenbrock C, Adorjan P, Grabs G, Lesche R, Leu J Lipscher E, Maier S, Model F, Mueller V, Otto T; Schwope I, Ziebarth H;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 28; SEQ ID 386; 117pp; English.
     ABZ10246 standard; DNA; 8056 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-MAR-2002; 2002WO-EP03401
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-MAR-2001; 2001US-27833P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (EPIG-) EPIGENOMICS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2003-018942/01.
                                                                                                                                                                                                                                                                                                                                                                                                   WO200277272-A2
                                                                                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                 16-JAN-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Lewin A,
Pelet C,
                                                           ABZ10246;
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                                                              GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC 1285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel shrunken seed gene useful for producing transgenic plants having altered production of food storage reserve material, intracellular transport of storage protein and formation of protein or oil bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GGTTAAGCGTTTTACTTATGGTTTATGCAACGGAAGAATATTGCCATTGTTGGAATGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence is that of Arabidopsis thaliana SSE1 (shrunken seed) cDNA, which was isolated from a seedling cDNA library using a partial genomic clone as probe. SSE1 encodes a protein (see AAB19/19) that, when expressed in a cell of a plant, modifies or alters the production of a food storage reserve material (e.g. protein, lipid or carbohydrate storage reserve), facilitates the intracellular transport of a storage protein, or facilitates the formation of protein or oil bodies. The invention provides a transgenic plant (or plant cell, plant tissue, plant organ or plant component) which includes a recombinant SSE1 transgene that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modifies the production of food storage reserves, thereby increasing nutritional value. An antisense construct is useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 242.4; DB 21; Length 1483; Pred. No. 3e-46; 0; Mismatches 1; Indels 0;
SSE1; shrunken seed gene; storage reserve; storage protein; oil body; transgenic plant; ss.
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                                                                                                                                         Location/Qualifiers
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1088 AGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAA 1147

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1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGAAAA 1330
  5687 ATTGAAATTTGATGATAATGATTGTGAGAATAATATTTGAAAATTTTTAATTGTTTAAA 5746
                                                                                                                                                                                                                                                                                                             (AAL07544-AAL26789) and methods of assessing whether a patient is affilted with breast cancer by examining the correlation between the expression of certain markers and the cancerous state of breast cells. The polynucleotides and encoded polypeptides are potential markers for detecting, diagnosing, monitoring, characterising treating and polynucleotides are constraint to the polynucleotides and encoded polypeptides are also useful for isolating compounds with cytostatic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention relates to human breast cancer expressed polynucleotides
                                                    TTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                                                                        ATTICATITIGGGAGIGIACIAGIAACIAGIAAGIACIAACIAACCAGAAIGAGIIICIGAIITI
                                                                                                                                                                                                             New peptide useful as a marker for the diagnosis of breast cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cancer expressed polynucleotide 8381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 1516; 3695pp; English.
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ID AAL15924 standard; cDNA; 422
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29-MAR-2000; 2000US-0193480
15-MAY-2000; 2000US-0205230
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2000US-0220534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14-JAN-2000;
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1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGAT 1267
                                                                                                                                                            1268 TTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAAAAGTATATTACTAAACAATAAAAAA 1327
                              1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTGTACAAAGCTA 1207
                                                             211 AAGNTITIANNANANATITINNNANNNTAAATITITINNTAAANANTAAANNCNTITITI 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to novel genes (AAH68727-AAH73383) associated with cervical cancer with cytostatic activity. The nucleic acids and encoded polypeptides are useful: to assess if a patient is afflicted with cervical cancer or has a pre-malignant condition; to monitor the progression of cervical cancer or a premalignant condition in a patient; and to assess the efficacy of a compound or therapy for inhibiting cervical cancer in a patient. The nucleic acids may also be useful for gene therapy.
                                                                                                                                                                                         92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cervical cancer, cytostatic, pre-malignant condition, gene therapy, ss.
   331 ATNNNTTTGAAAAAAAATANAAAAAANTTNGNNGGAATTAAAANAATTTTTTTNAAAA
                                                                                                                                                                                            New isolated nucleic acid for diagnosing and treating cervical car
and for assessing and detecting compounds for treating the cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 49; DB 22; Length 369;
Pred. No. 0.096;
0; Mismatches 144; Indels
                                                                                                                                                                                                                           1328 AAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCC 1367
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                                                                                                                                                                                                                                                          Human cervical cancer marker nucleic acid 818.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhao X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 242; 1051pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Berger A,
                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                        AAH69544 standard; cDNA; 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 44.4%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21-DEC-1999; 9908-0171350.
14-MAR-2000; 2000US-0189315.
12-MAY-2000; 2000US-0203791.
09-JUN-2000; 2000US-0210600.
21-JUL-2000; 2000US-0220114.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 2001-375006/39.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
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Gaps

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3.0%; Score 49.6; DB 22; Length 422; 42.1%; Pred. No. 0.072; cive 0; Mismatches 162; Indels 0

Conservative

Best Local Similarity Matches 118; Conserv

Query Match

0 other;

5401 A; 396 C; 5174 G; 9962 T;

Sequence 20933 BP;

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1270
                                                                                             1210
                                                                                                                                                                                                                                                                                     1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGAAAAA 1330
  TTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAAATC 1150
                                                                                                                                          194
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                                             TIGITAAAAAAAAAAAAAAAAGTINTTTTTCCGTAGGAAAAAATTTTTANTTTG
                                                                                             TTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                                                        253 ANTCCATCCNNGCATTGTTTTTANGTTTTTNCAGGCCGNNTNTTTGGANAAAAAGTNA
                                                                                                                                                                                        1211 ATTICATITIGGAGIGIACIAGIAACIAGIAAGIACIAACCAGAAIGAGITICIGAITIT
                                                                                                                                                                                                                                     1331 CATTTTGTGAAAAGAGAAA 1349
                                                                                                                                                                                                                                                                                                                                                                                                                                35
                                                                                                                                                                                                                                                                                                                                                                                                                             73 AAAAAAAAAAAAAAAAA
                                             313
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1091
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ESULT 6 BQ67124 D ABQ67124 standard; DNA; 20933 BP

ABQ67124;

28-AUG-2002 (first entry)

Human angiogenesis associated polynucleotide SEQ ID NO 154.

Human, angiogenesis, methylation, eye disease, glaucoma, tumour; inflammation, rheumatoid arthritis; diabetic retinopathy; antiulcerds, macular degeneration; inflammatory bowel disease, Crohn's disease, antirheumatic; antiarthritic; antidiabetic; antipsoriatic; antidiateriosclerotic; ds.

Homo sapiens.

10200246454-A2

13-JUN-2002.

06-DEC-2001; 2001WO-EP14320.

06-DEC-2000; 2000DE-1061338

(EPIG-) EPIGENOMICS AG

chacht O;

#PI; 2002-500450/53.

New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer

Claim 1; SEQ ID NO 154; 41pp + Sequence Listing; German.

The invention relates to a nucleic acid (I) comprising a segment of 18

bases of chemically pretreated DNA of anglogenesis-associated genes (II) having sequences (Abg66971-Abg67178) or their complements. (I), also related oligomers, are used to evaluate the methylation status and/or single-nucleotide polymorphisms, in anglogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy, eneovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabetic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and Crohn's disease.

Note: The sequence data for this patent did not form part of the printed

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Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
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1180 ITITITATAAATTAATAAAATAAATATTITITITAAGAAAAAATAGGTAAAGAATATAAATGG 1239
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                                                                     1091 TITITCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAAATTATTGAAAATC 1150
                                                                                                                                                                            1240 irranaaagararrrrrrrrrrangargrgaaaragrrarrrraararrarrarrang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (b) detecting a profile of expressed polymucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopais thallana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              printed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            e data for this patent is not represented in the printed is based on sequence information supplied to Derwent by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to identifying a stress condition to which a plant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses
                                                                                                                                          TITCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                     Gaps
Length 20933;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana; plant; gene; stress; transgenic; ds
                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana stress regulated gene SEQ ID NO 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2958 BP; 828 A; 621 C; 576 G; 933 T; 0 other;
                                                                                                                                                                                                              1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAA 1249
                                                                                                                                                                                                                                                   1300 Tritaagridggagrararaggraarrraaarrraaa 1338
   DB 24;
                                     69
 Score 48.6; DB
Pred. No. 0.32;
0; Mismatches
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(SYGN ) SYNGENTA PARTICIPATIONS AG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Note: The sequence data for this
                                                                                                                                                                                                                                                                                                                                         ABZ12533 standard; DNA; 2958 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang X,
 Query Match 2.9%;
Best Local Similarity 56,6%;
Matches 90; Conservative
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26-JAN-2001; 2001US-264647P.
22-JUN-2001; 2001US-300111P.
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                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2002-304127/34.
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                                                                                                                                                                           351
                                                                                                                                                                                                                                                                                                                                                                                                              290 GAGAAAGGTTTTTGTTGCAAATTAGTCATGAACTCACATTATCAAACGAGGTGAAATGAC 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 expressed sequence tag, lactation, LMFD, if at deposition; genome mapping, gene identification;
                                                                                                                                                                                                                                                                                  410 ATTAGCAACTAGCTAGTAATAAGTGTTTTTAGTTTTACAAGTATTTTACAGGGTTCTATC
                                                                                                                                                                                                                                   1288 ITAGGITAAAAAACAAGIATAITACTAAACAATAAAAGAAAAACAITITGIGAAAAAGA
                                                                                                                1228 ACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTTTGAAGCTTTTTC
                                                              Gaps
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      Length 2958;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  230 AAAACAATCCTTCGTTTGCAAGTTCAACAGTAGGCGAGACACTT 184
                                                           Indels
Score 47.8; DB 24;
Pred. No. 0.3;
0; Mismatches 112;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABX40620/c
ID ABX40620 standard; cDNA; 516 BP
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Query Match
Best Local Similarity 50.7%;
Matches 115; Conservative
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11-JAN-2000; 2000US-0480902,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (BYAT/) BYATT J C.
(MATH/) MATHIALAGAN N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2003-110599/10.
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WARREN W C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    deposition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ss; EST;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Syatt JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABX40620;
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1157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1278 GAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAACAATAAAAGAAAAACATTTTG 1337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA transcription associated gene; peptide nucleic acid; PNA-oligomer; PNA; cytosine methylation state; SNP; retroviral infection; gene; ds; single nucleotide polymorphism; adenosine deaminase deficiency; cancer; viral infection; Sezary syndrome; haematological disorder; tuberculosis; immunological disorder; Werner syndrome; developmental disorder; psoriasis; Rieger's syndrome; neurological disorder; erythropoiesis; neurodegenerative disorder; Mardenburg syndrome; Niemann-Pick disease; myelodysplastic syndrome; myocardial infarction; hypertension; arthritis; angiogenesis; congenital heart disease; HDR syndrome; gene therapy; polyglutamine disorder; solid tumour.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement or fragment) with a complementary nucleic acid molecule obtained from the bovine call or tissue, where hybridisation between the marker nucleic acid and the complementary nucleic acid permits the detection of the molecule, and (b) detecting the level or pattern of the complementary nucleic acid is predictive of the level or pattern of the molecule. The LWED nucleic acid is used for determining a level or pattern of a molecule in a bovine cell or tissue. It is useful for genome mapping, gene identification and analysis, cattle bredding, preparation of constructs for use in cattle gene expression, or for generically improving cattle. The present sequence is one of the 1512 bovine LMED EST (expressed sequence tag) nucleic acids.
nucleic acid (comprising any of the 15112 nucleic acid sequences or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1098 ATAAAATTAAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAAATCTTTCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1158 CCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGTATTTCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1338 TGAAAAGAGAAATAAAGTTTACTGGACCCCCATTGTACAGATGGTCCCATAATAATACTGA
                                                                                                                                                                                                                                                                            Note: The present sequence was not shown in the specification but was obtained in electronic format from the USPTO web site: seqdata.uspto.gov/sequence.html?DocID=20020137139.
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 46.6; DB 25; Length 516;
Pred. No. 0.37;
0; Mismatches 179; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                    Sequence 516 BP; 79 A; 14 C; 18 G; 403 T; 2 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA transcription associated genomic DNA #130
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ID ABK28385 standard; DNA; 7047 BP
                                                                                                                                                                                                                                                                                                                                                                                                               2.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                  46.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 46.2
Matches 154; Conservative
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AAS45323/c

06-DEC-2001

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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer; in particular an oligomuclectide or peptide nucleic acid (PNA)-oligomer that hybridises to or is identical to the chemically pretreated DNA of genes associated with DNA transcription. The set of oligomer probes are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleic acids are useful for diagnosing or treating diseases associated with DNA transcription (particularly with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary syndrome, thematological disorders, Menunological disorders, Warrer syndrome, thermorphopental disorders, postiasis, Rieger's syndrome, unemann-Pick disease, myclodysplastic syndrome, mycentension angiogenesic syndrome, mycentension angiogenesic syndrome, mycentension angiogenesic syndrome, solid tumours disease, HDR syndrome, arthitis, polyglutamine disorders, solid tumours associated genomic DNA molecules of the invention.

Note: The sequence AbK20127-AbK28472 represent DNA transcription associated denomic DNA molecules of the invention.

Note: The sequence data for this patent did not form part of the printed formed part of the printed forms between the format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1084 TTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATTATT 1143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer -
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49.7%; Pred. No. 0.8;
tive 0; Mismatches 146; Indels 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID No 259; 32pp; English.
                                                                                                                                                                                                                                                                                                                                                                      Berlin K;
                                                                          06-APR-2000; 2000DE-1019058.
07-APR-2000; 2000DE-1019173.
30-UJN-2000; 2000DE-1032529.
01-SEP-2000; 2000DE-1043826.
06-APR-2001; 2001WO-EP03973
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Best Local Similarity 49.7
Matches 145, Conservative
                                                                                                                                                                                                                                                                                                                                                                  Olek A, Piepenbrock C,
                                                                                                                                                                                                                                                                                   (EPIG-) EPIGENOMICS AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequences AAS45296-AAS45520 represent chemically pretreated genomic DNA molecules associated with the cell cycle-and specific PCR primers of the invention. The sequences are useful for detecting the methylation state of all CPG dinucleotides in a sequence and therefore for analysing associated diseases. By analysing oytosine methylations in the pretreated DNA, genetic and/or epigenetic parameters for the diagnosis and therapy of existing diseases or the predisposition to specific diseases can be ascertained. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The sequences of the invention are useful for the diagnosis and therapy of HIV infection, neurodegenerative disorders, graft-versus-host disease, arteriosclerosis, solid tumours and cancers.
                                                                                                                                                     Cell cycle; human; CpG dinucleotide; cytosine methylation; HIV; aging; human immunodeficiency virus; neurodegenerative disorder; solid tumour; graft-versus-host disease; glomerular disease; Lewy body disease; cancer; arthritis; arteriosclerosis; anti-HIV; neuroprotective; antiarthritic; immunosuppressive; antitumour; cytostatic; antiarteriosclerotic; ds;
                                                                                                                 Chemically pretreated complementary DNA associated with cell cycle #14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1088 AGCTITITICCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATTATIGAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1148 ATCTTTCCAACCATAGAAAGTTAAATTTGATCAGGGATGGAAATTTTTGTACAAAGCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Designing primers and probes for analysing diseases associated with eytosine methylation state e.g. arthritis, cancer, aging, arteriosclerosis comprising fragments of chemically modified genes associated with cell cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 17848;
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Pred. No. 1;
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AAS45323 standard; DNA; 17848
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Similarity 45.6%;
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07-APR-2000; 2000DB-1019173.
30-JUN-2000; 2000DB-1032529.
01-SEP-2000; 2000DB-1043826.
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                                                                              (first entry)
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                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                        PCR primer.
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9927 ATAAAATAACTAAAATTAAAAAAAAAATATAATATTTAACATTTTTAATTTTTCTTTT
                                                                   1388 ATAATACTGATAGAAGATAGAGAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAAT
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ВЪ ABK39976 standard; DNA; 17848 RESULT 11 ABK39976/c

ABK39976

(first 21-MAY-2002 Human chemically pretreated gene sequence #29 strand 2.

treatment; CpG; DNA methylation; cancer; tumour cytostatic, ALDH6; CYP11A; CYP11B1; CYP3A3; Driv, Driv, CYP11BH1; UGT8; MRP; pharmacogenomics; SNP; single mucleotide polymorphism. Human; ds; bisulphite

Homo sapiens

WO200202806-A2

10-JAN-2002

29-JUN-2001; 2001WO-EP07470

30-JUN-2000; 2000DE-1032529 01-SEP-2000; 2000DE-1043826

(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

Berlin K;

WPI; 2002-154757/20

New nucleic acid, oligonucleotides and peptide nucleic acid-oligomers, useful for detecting cytosine methylation state of genes associated with pharmacogenomics and for therapy of diseases e.g. cancer

Claim 1; SEQ ID No 58; 24pp; English

The invention relates to a nucleic acid comparising a sequence at least 18 bases in length of a segment of the chemically pretreated DNA of genes associated with pharmacogenomics according to one of the cequences of the genes ALD pharmacogenomics according to one of the sequences of the genes ALD pharmacogenomics according to one of the sequences of the genes ALD NR 000593, CYP1A (NM 000491), CYP1B1 (NM 000497), CYP3A3 (NM 005939, TXNRD1 (NM 001979), CCLM (NM 001979), CCLM (NM 001979), CCLM (NM 0019901, NM 019862, NM 019862, NM 019862, NM 019862, NM 019869, NM 019869, and their complements. The chemical pretreatment for shell pharmacolles (SI) chosen is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an is bisulphite treatment to convert cytosines (but not methyl-cytosines) into uracils. Also included are an oligomer (II) in particular an oligomer, comprising in each case at least one base sequence having a length of 9 nucleotides which hybridises to or is identical to a chemically pretreated DNA of genes associated with the methylation state (CpG) and/or detecting SNPS (single nucleotide polymorphisms) an array for analysing diseases associated with the methylation state (CpG) and/or detecting SNPS (single nucleotide polymorphisms) coff the 87 sequences. The oligomers may also be used as PCR primers: The set of 87 nucleic acids and their complements is useful for diagnosis and therapy of solid tumours and cancer. The present sequence

2000DE-1019173 2000DE-1032529

06-APR-2000; 07-APR-2000; 30-JUN-2000; 01-SEP-2000;

2000DE-1043826

(EPIG-) EPIGENOMICS

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                                                                                                                                                                                                                                               1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTA
                                                                                                                                                                                                                                                                           1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAGTACTAACCAGAATGAGTTTCTGAT
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                                                                                                                                      Gaps
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       of the printed specification, but was obtained in electronic format directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA transcription associated complementary genomic DNA #19.
                                                                               6 other
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                                                                              Sequence 17848 BP; 5055 A; 211 C; 3533 G; 9043 T;
                                                                                                                                    0; Mismatches 196;
                                                                                                        Score 46.4;
Pred. No. 1;
                                                   ftp.wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
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Similarity 45.6%;
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                                                                                                        Query Match
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Haematopoietic cell proliferation disorder related DNA sequence #386

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Berlin K;

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New nucleic acids or oligomers, useful for diagnosing or treating diseases associated with DNA transcription, e.g. immunological disorders, Werner syndrome, psoriasis, myocardial infarction, solid tumours or cancer
                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID No 38; 32pp; English
Piepenbrock C,
                                                                     WPI; 2002-090046/12
olek A,
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The invention relates to a nucleic acid, which comprises a segment of the chemically pretreated DNA of genes associated with DNA transcription from one of 346 sequences, and an oligomer that hybridises to or is identical to peptide nucleic acid (PNA) -oligomer that hybridises to or is identical transcription. The set of oligomer probes are useful for detecting the transcription. The set of oligomer probes are useful for detecting the crimically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically pretreated genomic DNA. The nucleotide polymorphisms (SNPs) in a chemically with the methylation status), e.g. adenosine deaminase deficiency, viral infection, retroviral infection, Sezary Syndrome, haemacological disorders, immunological disorders, where syndrome, neurological disorders, immunological disorders, wardenburg syndrome, Niemann-Pick disease, myelodysplastic syndrome, myocardial infection, hypertension, anglogenesis, erythropolesis, companital heart disease, HDR syndrome, arthritis, polyglutamine disorders, solid tumours or cancer. Sequences ABK28127-ABX28472 represent DNA transcription associated genomic DNA molecules of the invention.

Subscribed and for this patent did not form part of the printed specification but was obtained in electronic format directly from the

Sequence 17848 BP; 5055 A; 211 C; 3533 G; 9043 T; 6 other;

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9747 AAATCTATTACCCAATAAAAAATAATTAATCTTAACTAAAAACACAATTCATCCTAAT 9688
                                                                                                                                                                                                                                                                         10047 ААСТПАААААААСААТПТТААААТТТТААААТТААААТТААААДССТААТТААТАТАТААТТСАА 9988
                                                                                                                                                                                                                                                                                                                                                                                                                                                      9987 Адалалалалалалалалалаланталатталапалалалаттттталалалалалатс 9928
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9927 АТААААТААТААСТААААТТАААААААААТАТАТАТАТТТААСАТТТТААТТТТАТТТТ 9868
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1268 ITTGGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAAACAATAAAAGAA 1327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAACATTTTGTGAAAAGAGAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCATA 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1088 AGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAA
                                                                                                                                                                                                                                                                                                                                                                  1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1388 ATAATACTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAATCGGAAT
                                                                                                 0; Gaps
         DB 24; Length 17848;
Query Match
2.8%; Score 46.4; DB 24; Length 1
Best Local Similarity 45.6%; Pred. No. 1;
Matches 164; Conservative 0; Mismatches 196; Indels
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ABZ10246 standard; DNA; 8056

RESULT 13 ABZ10246/c

(first entry)

16-JAN-2003

ABZ10246;

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differentiating between harmatopoietic cell proliferative disorders associated with at least 1 gene and/or their regulatory regions in a subject. The method comprises contacting a target nuclaic acid in a biological sample obtained from the subject with at least 1 reasont, which distinguishes between methylated and non-methylated CpG dinucleotides within the target nucleic acid. AE209861 to AE211118 circleotides within the target nucleic acid. AE209861 to AE211118 circleotides within the target nucleic acid. AE209861 to AE211118 circleotides within the target nucleic acid. AE209861 to AE211118 circleotides within the target nucleic acid. AE209861 to AE211118 circleotides within the target nucleic acid. AE209861 to AE211118 circleotides within the larget nucleic acid. AE209861 to AE211118 circleotides within the larget nucleic acid. AE209861 to AE21118 circleotides and acute myelogenous leukaemia, as probes for disorder haematopoietic cells for differentiating between acute lymphocytic leukaemia and acute myelogenous leukaemia, as probes for determining the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) of haematopoietic cell proliferation disorder related sequences and their complements; and as primers for the amplification of haematopoietic cell proliferation between subclasses, diagnosis, prognosis, treatment and/or monitoring of haematopoietic cell proliferative disorders. The present method enables chaematopoietic cell proliferative disorders. The present method enables a highly specific classification of haematopoietic cell proliferative disorders. The present method enables contacras allowing for improved and informed treatment of patients.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Detecting and differentiating between hematopoietic cell proliferative disorders, comprises contacting a target nucleic acid with a reagent that distinguishes between methylated and non-methylated CpG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1137 AATTATTGAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1257 GAGTITICIGATITITIGGATITITICAAGCTITICITIAGGTIAAAAAAAGAAGTATAATAAAA
                                     Human, haematopoietic cell proliferation disorder, cytostatic; gene therapy, lymphocytic leukaemia, acute myelogenous leukaemia; cytosine methylation state; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                        ve A, Mueller J;
Lesche R, Leu E;
ller V, Otto T;
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2.7%; Score 46; DB 25; Length 8056;
Best Local Similarity 50.5%; Pred. No. 1;
Matches 112; Conservative 0; Mismatches 110; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present invention describes a method for detecting and
                                                                                                                                                                                                                                                                                                                                                                                                                        i, Braun A, Distler J, Guetig D, Howe A, M
Piepenbrock C, Adorjan P, Grabs G, Lesche I
Lipscher E, Maier S, Model F, Mueller V,
Schwope I, Ziebarth H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 8056 BP; 3711 A; 0 C; 371 G; 3974 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 28; SEQ ID 386; 117pp; English
                                                                                                                                                                                                                                                                                   26-MAR-2002; 2002WO-EP03401.
                                                                                                                                                                                                                                                                                                                                   26-MAR-2001; 2001US-278333P.
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Schwope I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-018942/01.
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                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                        03-OCT-2002.
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Pelet C,
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RESULT

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WPI; 2002-154758/20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200202807-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JUL-2002
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                                                     1304
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                                                                                                     15592
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ਨੇ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             15653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1124 CCTAACCAATAAAATTATTGAAAATCTTTCCAACCATAGAAAAGTTAAAATTTGATCAGC 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1184 GATGGAAATTTTTGTACAAAGCTAGGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAG 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inflammation; rheumatoid arthritis; diabetic refinopathy; antiulcerds; macular degeneration; inflammatory bowel disease; Crohn's disease; antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New nucleic acid fragments from chemically treated angiogenesis-associated genes, useful for determining methylation status, e.g. in diagnosis or treatment of cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis and treatment of eye diseases, proliferative retinopathy, neovascular glaucoma, solid tumours, inflammation, rheumatoid arthritis, diabbtic retinopathy, macular degeneration caused by neovascularisation, psoriasis, arteriosclerosis, inflammatory bowel diseases, ulcers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a nucleic acid (I) comprising a segment of 18 bases of chemically pretreated DNA of angiogenesis-associated Genes (II) having sequences (ABQ66971.ABQ67178) or their complements. (I), also related oligomers, are evaluate the methylation status and/or single-nucleotide polymorphisms, in angiogenesis-related genes, for diagnosis and treatment of eye diseases, proliferative retinopathy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 37515;
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                                                                                                                                                                                                                                                                                                                                                Human angiogenesis associated polynucleotide SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 45.6; DB 24; Length
Pred. No. 1.8;
0; Mismatches 129; Indels
1317 CAATAAAAGAAAACATTTTGTGAAAAGAGAAATAAAGTTTA 1358
                                                     Claim 1; SEQ ID NO 28; 41pp + Sequence Listing; German.
                                                                                                                                                                                                                                                                                                                                                                                                            methylation; eye
                                                                                                                                                                                        ABQ66998 standard; DNA; 37515 BP.
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larity 48.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-2001; 2001WO-EP14320
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-DEC-2000; 2000DE-1061338
                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antiarteriosclerotic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2002-500450/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (EPIG-) EPIGENOMICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200246454-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                28-AUG-2002
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Matches 123;
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Best Local
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ABQ66998/c
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The invention relates to a nucleic acid comprising a sequence of at least 18 bases of a segment of chemically pretreated DNA of genes associated with cell signalling. The activity of the modified sequences of the invention may be described as cytosfactic. The object of the invention is to provide the chemically modified DNA of genes associated with cell capability as well as oligonacleotides and/or PNA-oligomers for detecting cytosine methylations, as well as a method which is particularly suitable for the diagnosis and/or therapy of genetic and particularly modified DNA provided by the invention is useful for diagnosis of interapy of diseases such as sociated with cell signalling. The chemically modified DNA provided by the invention is useful for diagnosis of interapy of diseases such as sociat them and cancer. The sequences given in records ABL70111-ABL7065C represent chemically pre-treated genomic DNA's of genes associated with cell signalling of the printed specification, but is based on sequence information supplied by the Interpretation better office.
                                    15593
                                                                                                                                                                          15533
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               294 TTAAAAAAATCATAAATCATCTACTATAAAAATAAAACAAACATTCATAAACAAACA 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid, useful for diagnosis and therapy of diseases associated with cell signalling e.g. cancer, comprises chemically modified genomic sequences of genes associated with cell signalling -
                                 GTATATTACTAAACAATAAAAAAAAAAAACATTTTGTGAAAAAGAGAAATAAAGTTTACTGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cytosine methylation; cell signalling disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 6352;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1, SEQ ID NO 453; 24pp+sequence listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chemically treated cell signalling DNA sequence#227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2.7%; Score 45.4; DB 24;
31.4%; Pred. No. 1.3;
ve 0; Mismatches 121;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytostatic; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ABL70563 standard; DNA; 6352
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Matches 131; Conservative
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01-SEP-2000; 2000DE-1043826.
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1161 TAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAACCTAGGTATTTCATTTG 1220
234 AAAAAAAAAAAAAACATTAAAAATAAAAAAAAAGGAAAAAACGATCTATTAATAATA 175
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1280		A 115
ATTTTGGATTTTGAA 1280	=	ATTCTCTAATATTCTAAA 115
AGAATGAGTTTCTG	_	AATTTTTAAAATT
PAGTAAGTACTAACC	=	AATCTATTAATAAAT
1221 GGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTTGG		174 TCTCTAAACTTTATCAAATCTATTAATAATAATTTTTTAAAATTCTCTAATATTCTAA
1221		174

Search completed: February 1, 2004, 21:58:56
Job time : 496.261 secs

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FEATURES

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/clone="GK-205F06-014511"
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                                                                                                                                                                                                                                                                                             directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used ca be found at http://signal.salk.edu/tdna_protocols.html" 75 c 51 g 105 t
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/strain="columbia 0"
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/db xref="taxon:3702"
/clone="SALK 026421.45.45.x"
/clone="SALK 026421.45.45.x"
/clone="RATADIdopsis thaliana TDNA insertion lines"
/note="TPCR was performed on Arabidopsis thaliana lines
/note="TPCR was performed on Arabidopsis thaliana lines
elements. The resultant fragment for each line was
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                     border of end of
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(flanking sequence tags) from Arabidopsis thaliana T-DNA
transformed lines
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0
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                     This is single pass sequence recovered from the left TDNA, This sequence lies within 300 bases of the 5' e
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                                                                                                                                                                                                                                                                                                                                                                                                             Score 295.4; DB 29;
Pred. No. 1.5e-38;
0; Mismatches 1;
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Arabidopsis thaliana
                                       enomic survey sequence
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ilarity 99.7%;
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     ecker@salk.edu
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/clone_lib="Arabidopsis thaliana T-DNA insertion lines"
/clone_"PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryochyta, Embryophyta, Tracheophyta;
Bukaryochyta, Viidiplantae, Streptophyta, Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta, eudicocyledons, core eudicots, rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (Dases II to 278)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P.
                     Zuechtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany This sequence is recovered from the left border of the T-DNA. It indicates an insertion within the locus defined by clone f418. The sequences are generated at the MPI for Plant Breeding Research in the context of the GABI-Kat project. GABI-Kat is part of the German Plant Genomics program designated 'GABI'. Information on line availability can be found at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               624
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Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14.7%; Score 246.8; DB 29; 99.2%; Pred. No. 1.4e-30; tive 0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                 http://www.mpiz-koeln.mpg.de/GABI-Kat/.
Location/Qualifiers
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, endicotyledons, core eudicots, rosids
; eurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 232)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BH612074 232 bp DNA linear GSS 04-JAN-2002 SALK 032102 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_032102, genomic survey sequence.
sequence tags from normalized and
                                                                                                               Contact: Erika Asamizu
The First Laboratory for Plant Gene Research
Assusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 TITITCAGAICATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 GAAATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gadrinab
                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two
six-week old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 TTTTTCAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GABATTGTGTTTTTTGCBACAGGTAGAGAGCATAACCATAGACAGATGTATCTGAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241 GGTTAAGCGTTTTACTTATGGTTTATACGAACGGAAGAATATTGCCATTGTTGGAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 TAAGCTTCTCTACGCCTAAAGAATGGACCGATACGAATAAAACAAAATCATTAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Ge, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                      'tissue_type="aboveground organs"
                                                                                                                                                                                                                                                                               organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 233; DB 9;
Pred. No. 2.4e-28;
0; Mismatches 5;
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of 12,028 non-redundant expressed
size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:3702"
clone="APZ63b12F"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54 9
                                                                                                                                                                                                                                                                                                             mol_type="mRNA"
strain="Columbia"
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BH612074.1 GI:18059525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.9%;
ilarity 97.9%;
Conservative
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g
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Best Local Similarity
Matches 236; Conserv
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                                                                                                  10907847
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BH612074/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases 1 to 347)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1540 ATATATATCCTGACGAGTCACATTTAGTAATCTCCTTGGACGTGTAAACGCCGTTAAAA 1599
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cGTTGATTTTTCCCGCATCAAAAACGTTGAATACTATTCTCACATGATTTCCTGCTCCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ATATATATATCCTGACGTCACATTTAGTAATCTCCCTTGGACGTGTAACGCCGTTAAAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:3702"
/clone="SAIK 106185.39.30.x"
/clone="SAIK 106185.39.30.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GATTIGATCACGIGGTACAATCGGAGATGGATCTTTATAGCTCATCCAACACACATGAGAG 60
                                                                                                                                                                                                                                                            This is single pass sequence recovered from the left border of TDNA. This sequence lies within 300 bases of the 5' end of AL2945680.
Class: TDNA tagged.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 cááriciriroccárigiáricogorriraacaacrorogicárcarorocacogrofi
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    Ecker,J.R.
Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CGTTGATTTTTCCCGCATCAAAAGCGTTGAATACTATTCTCACTTGTTT
                                                                               Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 858 553 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 233.2; DB 29;
Pred. No. 2.3e-28;
0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="genomic DNA"
strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                      TDNA tagged.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13.9%;
ilarity 96.5%;
Conservative
    Zimmerman, J. and
Sequence-Indexed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
69
                                                      Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1421 GATTIGITCACGIGGIA
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                                                                          Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          249;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S:
Matches 249
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NV521636/c
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FERSION
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AUTHORS
TITLE
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Shinn, P.

us-09-938-842a-3729.rst

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organism="Arabidopsis thaliana"
'mol_type="genomic DNA"
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/db xref="taxon:3702"
/clone="RAFL07-08-P04"
                                /mol_type="genomic_D
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AV825375.1 GI:19867435
                                                                                                                                                                                                                                                                                      Match 9.8%;
Local Similarity 97.7%;
les 167; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Motoaki Seki
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O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
AV825375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                npublished
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                                                                                                                                                                                                                                                                                          Query Match
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Matches
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AUTHORS
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JOURNAL
COMMENT
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AV825375
LOCUS
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KEYWORDS
SOURCE
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               188 AGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAAACAAGCATCATTAAAGATTA 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 AATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAGTGAAAGTAA 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spernatophyta, Magnollophyta, eudicocyledons, core eudicots, rosid, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

    (bases 1 to 233)

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 AATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAGTGAAAAGTAA 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               183 AGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGATTA
               10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of TDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           303 AAACATCGGAATCCAAAACCTCAAATTTACCAATCAGCCCAAATTATTGAT 353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAACATCGGAATCCAAAACCTCAAATTTACCAATCAGCCCAAATCTGTAAT 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 232;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 W. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                          28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4,
Studies
                                                                                                                                                                                organism="Arabidopsis thaliana'
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 164.6; DB
Pred. No. 4e-17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
The Salk Institute for Biological
                                                                                                                                                                                                                                      db_xref="taxon:3702"
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                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                  /mol_type="genomic"
/strain="Columbia 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 97.7%;
Matches 167; Conservative
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                                                                                                                         Class: TDNA tagged
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Email: ecker@salk.
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BH612075/c
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Email: mseki@rtc.riken.go.jp
An Arabidopsis full-length oDNA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified.Lambda FLC-1 vector (Carnincl et
al., submitted for publication) digested with BamHI and SalI. This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AV825375 AFL7 Arabidopsis thaliana cDNA clone RAFL07-08-F04 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               core eudicots; rosids
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
spermatophyta; Magnoliophyta; endicotyledons; core eudicots; rosid;
lossid II; Brassicales; Brassicaces; Arabidopsis.

Seki, M., Narusaka, M., Ishida, J., Kamiya, A., Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Shibata, K., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
/db_xref="taxon:3702"
/clone="SALK 032104"
/clone="SALK 032104"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana lines
notes"PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         128 AATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTGGTAAAGTAA
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 164.6; DB 28;
Pred. No. 4e-17;
0; Mismatches 4;
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us-09-938-842a-3729.rst

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1656 GITTICICICAGCIATATITIA 1677
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Location/Qualifiers
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BH617024.1 GI:18427119
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Fax: 858 558 6379
Email: ecker@salk adv
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                    1588 ACGCCGTTAAAACGA7
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Best Local Si
Matches 82
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BH493162/c
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AUTHORS
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BH617024
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                                                                                                                                                                                                               1577 ITGGACGIGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTC 1636
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ept. of Biochemistry & Molecular Biology
Lichigan State University
24 Biochemistry, Michigan State University, East Lansing, MI 48824
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosic;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Thite, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de larduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.

An new set of Arabidopsis expressed sequence tags from developing seeds: The metabolic pathway from carbohydrates to seed oil lant Physiol. 124 (4), 1582-1594 (2000)
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|note="Organ: Developing seed, Vector: pBluescript SK-;
|site_l: EcoRl; Site_2: XhoII"
| 97 c 81 g 92 t
                                                                                                                                                                                                                                                   TTGGACGTGTAACGCCGTTAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Michigan State University DNA Sequencing Facility Arabidopsis Biological Resource Center, The Ohio State University, 309 Bot Scology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
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                                             SalI; subjected hr)"
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                                                                                                                                            Length 486;
                                                                                     3 others
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dev_stāge="5-13 days after flowering"
lab_host="E.coli"
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                                                                                                                                          DB 9; L
8.2e-07;
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                              /clone_lib="RAFL7"
/note="Site 1: BamHI; Site_2:
cold_treated (1, 2, 5, 10, 24 11) t
118 c 117 g 117 t
dev_stage="rosette plants"
'lab_host="DH10B"
                                                                                                                                        6.0%; Score 101; DB
100.0%; Pred. No. 8.2
:ive 0; Mismatches
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Arabidopsis thaliana
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strain="Columbia"
db_xref="taxon:3702"
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Fax: 517 353 9334
Email: benning@msu.edu
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Best Local Similarity 100.
Matches 101; Conservative
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Best Local Similarity
Matches 88; Conserv
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Eukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots, rosids,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
CGTCATCTC 1647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (bases 1 to 146)
Alonso, J.M., Leisse, T.J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Jeske, A., Karnes, M., Kim, C.J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             directly sequenced to determine the genomic sequence at the site of insertion, Details of the protocols used can be found at http://signal.malk.edu/tdna_protocols.html"
                                                                                                                                                                                                                                                                                                                                                                              TDNA insertion lines Arabidopsis
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/clone="sALK 035853"
/clone=lb="Arabidopsis thaliana TDNA insertion lines"
/note="pcK was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultent fragment for each line was elements.
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thallana genomic clone SALK_035853, genomic survey sequence.
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Class: TDDM tagged.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
                                                                                                                                                                                                                                                                                                                                                linear
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/mol_type="genomic DNA"
/strain="Columbia 0"
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Pred. No. 0.0014;
                                                         13 ACGAGGTTAAAACGATTCTTTCCCATTGTATCCGCT
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100.0%; Pred. No. v...
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RESULT 12
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DEFINITION
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Brassica oleracea
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermacophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 825)
Town, C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
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BONGW95TF BO 1.6 2 KB tot Brassica oleracea genomic clone BONGW955,
BRAANER
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1 (bases 1 to 735)
1 (bases 1 to 735)
1 Youn, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M. Whole genome shotgun sequencing of Brassica oleracea Unpublished
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                                          GSS 13-DEC-2001
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825 bp DNA linear GSS 13-DEC-:
BCGCH91TR BCGC Brassica cleracea genomic clone BCGCH91, genomic
SULYCHY SEQUENCE.
BH493162
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/clone="BOGOH91"
/clone="BOGOH91"
/clone="BOGOH91"
/clone="BOGOH91"
/clone="BoGOH91"
/clone="Woctor: phOS1; Site 1: BstXI; 2-3 kb sheared
/note="Woctor: phOS1; Site 1: BstXI; 2-3 kb sheared
/note="Woctor: phOS1; Site 1: BstXI; linkers"
/clone="Bogoh91"
/cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-3523 Fax: 301-838-3520 Fax: 301-83-3520 Fax: 301-83-3520 Fax: Seq primer: Trom a doubled haploid provided by Tom Osborn. Seq primer: Trom a Location/Qualifiers
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/strain="TO1000DH3"
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Contact: Chris Town
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BX364179 Homo sapiens B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED Homo sapiens CON CSODL010XC24 5-PRIME, mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          224 AAGGACG-----ATAGGATGTTGGAGCCCAGG--AGAGGATTATTCCAAAGACACTAA 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              844 TTACAATCATTTCGATTACTTTGATCTGATTTCTAGTTTCGGTTTGTATGTTTAATATCCG 903
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="BONCW95" 2 KB tot" /clone 11b="BO 1.6 2 KB tot" /nclone 11b="BO 1.6 2 KB tot" /nclone="Vector: pHOSI; Site 1: BstXI, 1.6-2 kb sheared cotal DNA inserted into pHOSI using BstXI linkers" total DNA inserted into pHOSI using BstXI linkers" 94 c 148 g 241 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  904 GATTGTACAAGTACACAAGTACATAAGTATG--CGTATATGTATGTGACCGGTTTAATCA
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BP 191 91006 BVRY cedex - France
Email: seqrefegenoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 3188:
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 3.9%; Score 64.6; DB 29; Length 735;
Best Local Similarity 62.3%; Pred. No. 0.66;
Matches 195; Conservative 0; Mismatches 94; Indels 24;
                                                                                                                                                                           provided by Tom Osborn
                                           MD 20850, USA
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TIGR Medical Center Drive, Rockville, MD 9712 Medical Center Drive, Rockville, MD Fel: 301-838-0208
Fax: 301-838-0208
Fmail: cdtown@tigr.org
DNA is from a doubled haploid provided bo Seq primer: IF
Class: bheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
/db_xref="taxon:3712"
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A Sequence-Indexed Library of Insertion Mutations in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /mol_type="mRNA"
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/db_xref="taxon:960"
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/cell_type="B CELLS (RAMOS CELL LINE) COT 25-NORMALIZED"
/cell_line="RAMOS CELL LINE"
                                                                                                                                                                                                                                                                                                                                                     /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V attes of the pcMYSPORT 6 vector. Library was normalized. 128 c 121 g 449 t 156 others
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CSODL010BB12QP1&cluster=3185.r. Contact
cgi-bin/cluster.cgi?seq=CSODL010BB12QP1&cluster=3185.r. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
Faraday Avenue Genoscope sequence ID : CSODL010BB12QP1.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Arabidopsis thaliana
                                                                                                                                                                    organism="Homo sapiens"
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CC459772
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1C459772/c
JOCUS
DEFINITION
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ORGANISM
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FERSION
CEYWORDS
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BX335665
BX335665 Homo sapiens PLACENTA COT 25-NORWALIZED Homo sapiens CDNA clone CSODI017X104 5-PRIME, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /cloude libe. Attablidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used car
found at http://signal.salk.edu/tdna protocols.html*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Mammalia; Eutheria, Primates, Catarrhini, Hominidae, Homo,
1 (bases 1 to 1201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1057 TAATGGGGTCCAACCCCAAGTATGGGCTTACAGCTTTTTCCATAAAATTAAAGT----AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    475 TAATGGGGTCCAACCCCAAGTATGGGCTTACAGCTTTTTCTCTCATAAATATTAGAAGTAAG
                                                                                                                                                                                                                                                                                                This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact : Feng Liang Email : fllang@lifetech.com URL : http://fulllength.invitrogen.com/ InvitroGen Corporation 1600 Faraday Avenue Genoscope sequence ID : CSODIO17DE02QF1. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: secref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 7077.f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 600;
                                                     Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
THE: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                16; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             415 Arcitititadecerarecaaraaaariaregaaarcitraceae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 63.4; DB 29;
Pred. No. 1.1;
0; Mismatches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Arabidopsis thaliana"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="SALK 133376.34.05.x"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
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Conservative
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dopsis Genome
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                                                                                                                                                                                                                                                                                                                                          1084 TTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAATTATT 1143
                                                                                                                                                                                                                                                                                                                                                                                                                                         1203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="PLACENTA COT 25-NORMALIZED"
/clone_lib="Hdmo sapiens PLACENTA COT 25-NORMALIZED"
/note="list strand cDNA was primed with a NoII-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and BcoR vides of the pCMVSPORT 6 vector. Library was normalized
sites of the pCMVSPORT 6 vector. Library was normalized.
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Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 6537.f For
more information about this cluster, see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.genoscope.cns.fr/
cgi.bin/cluster.cgi?seq=CLOBB029ZG02FP1&cluster=6537.f. Contact
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitroden Corporation 1600
Faraday Avenue Genoscope sequence ID : CLOBB029ZG02FP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WATITITITITIANIWAAAAAWAAAAAWWAAAAAWWIWWWITIAYITAAATITIAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                         1144 GAAAATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     965 AAAAAATACCYCCAKAAAAAAATTTAAAAAATTYTAAWAAAAAATTTTCAACAWA
                                                                                                                                                                                                                                                                                           2; Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                          Length 1201;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1444 GAATGGTTCTTTAAAGCTCATCGAACACATCAGGACCGTTGATTTT 1490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          i, W.B., Gruber, C., Jessee, J. and Polayes, D. ull-length cDNA libraries and normalization
                                                                                                                                                                                                                                          Query Match 3.7%; Score 62.6; DB 13;
Best Local Similarity 37.8%; Pred. No. 1.2;
Matches 154; Conservative 63; Mismatches 188;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Genoscope
Genoscope - Centre National de Sequencage
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clone="CS0DI017YJ04'
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KEYWORDS
SOURCE
ORGANISM
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BX404443/c
LOCUS
                                                                                                                                                                  BASE COUNT
ORIGIN
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AUTHORS
TITLE
JOURNAL
COMMENT
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/organism="Homo sapiens"

/mol_type="mRNA"

/db_txref="taxon:9606"

/clone="Cloud type="NEUROBIASTOMA"

/tissue_type="NEUROBIASTOMA"

/clone lib="Homo sapiens NEUROBIASTOMA"

/clone lib="Homo sapiens NEUROBIASTOMA"

/note="Vector: pCW/SPORT 6; lat strand cDNA was primed note="Vector: pCW/SPORT 6; lat strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoRV sites of the pCMVSPORT 6 vector.

Library was not normalized " 194 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1219 TGGGAGTGTACTAGTAACTAGTACTAACCAGAATGAGTTTCTGATTTTGGATTTTG 1278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1279 AAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGAAAAACATTTTGT 1338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   308 TAAAMCCAAAWTATAKATTTTTTTTAATATAAAAATATTTTTTCCYAATTTTTTAWWAAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                   Length 936;
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                                                                                                                                                                                                                                                                                                                                                                                                                         3.5%; Score 59.4; DB 13;
ilarity 47.1%; Pred. No. 4.4;
Conservative 17; Mismatches 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1099 TAAAATTAAAGTAAATCTTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Simi
Matches 120;
                                                                                                                                                                                                                                                                                                                                 BASE COUNT
ORIGIN
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02:56:40 2, 2004, Search completed: February Job time : 3887.05 secs us-09-938-842a-3729.rni

Sequence 25, Sequence Sequence Sequence

Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

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APPLICATION NUMBER: EP 91 114 300.6
PILING DATE: 26-AUG-1991
ATTORNEY/AGRAT INPORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 39,768
REPRERNCE/DOCKET WUMBER: 30472/114 IMMU
TELEPHONE: (703)836-9300
TELEPAX: (703)683-4109
                                                                                                                                                                                                                                                                   ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2.8%; Score 46.4;
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ) IMMEDIATE SOURCE:

CLONE: pTZgpt-F1s

US-08-232-463-14
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                                                                              1, 2004, 21:45:16; Search time 110.457 Seconds (without alignments) 6701.220 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                  1 ggttaagcgttttacttatg.......tttctctctagctatatttta 1677
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Sequence 1,
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Sequence 163
Sequence 233
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: /cgn2_6/ptodata/2/ina/5B_COMB.seg:*
: /cgn2_6/ptodata/2/ina/5B_COMB.seg:*
: /cgn2_6/ptodata/2/ina/6A_COMB.seq:*
: /cgn2_6/ptodata/2/ina/6B_COMB.seq:*
: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
: /cgn2_6/ptodata/2/ina/PacKfIles1.seq:*
 5.1.6
Compugen Ltd.
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                                                                                                                                                                                                                                                             of hits satisfying chosen parameters:
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US-08-232-463-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -826B-13
                                                                                                                                                                                                                                   569978 seqs, 220691566 residues
GenCore version (c) 1993 - 2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                     nucleic search, using sw model
                                                                                                                                                                                           IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                    US-09-938-842A-3729
1677
                                                                                                                                                                                                                                                                                          Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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2169 4
606 /
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2251
64976
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33385
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7218
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19124
731
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2341
             Copyright
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                                                                                                                                    Title:
Perfect score:
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37.6
37.6
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                                                                                                                                                                                                                                                               Total number
                                                     OM nucleic
                                                                                                                                                                                                                                                                                                                                                                                           Database :
                                                                                                                                                                  Sequence:
                                                                                                                                                                                                                                    Searched:
                                                                                 Run on
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Length 7218; STATE: VA
COUNTRY: USA
ZUB: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
PRICK APPLICATION DATA:
APPLICATION NUMBER: US/0935,313
FILING DATE:
PILING DATE: Sequence 14, Application US/08232463
Patent No. 5570367
GENERAL INFORMATION:
APPLICANT: BORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500 DB 1;

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138 AACAGGTAGAACATAACCATAGACAGATGTATCTGAAGAGATAAGCTTCTCTATGTCT 197
                                                                                                                                             198 AAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGATTAAATGGTTTGTAAGAA 257
                                                                                                                                                                                                                             378 ATGGTAGGCAAAAGTTGGTGGCTGCGAAAATTACAACATTATCCCTCTGTGGTGGACCCG 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1028 AATTCTGTGAGCGTATGGCAAACGAAGGAAAATAGTTATAGTAGCGCACTCGATGGGA 969
                                                                                                                                                                           18 SPRERERRERRERRERRERRERRERRERATICGCAAGCTCCCTCGACCTGCAGCCAAGCTCGGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Retroviral Vectors for Transducing
Beta-Globulin Gene and Beta-Locus Control Region
Derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            438 AATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTTAAGCCTAAAAGGTTACT
                          Gaps
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Best Local Similarity 12.9%; Pred. No. 0.019;
Matches 59; Conservative 189; Mismatches 210; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          558 AATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTT 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  968 cárricáácgraaaccgriraarááráririrgaarcri 931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          URRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/076,090
FILING DATE: 19930611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3: Kilpatrick & Cody
1100 Peachtree Street, Suite 2800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT 6128
THE COMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   equence 1, Application US/08076090 atent No. 5631162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LeBoulch, Philippe
London, Irving M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tuan, Dorothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Ret
TITLE OF INVENTION: Bet
TITLE OF INVENTION: Bet
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSED: Kilpatrick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: U.S.
ZIP: 30309-4530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Atlanta
                                                                                                                                                                                                                                                                                                             318
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1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATTATTACTAAAAAATAAAAGAAAA 1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                744 AATTGAAAATAAAAGAAATAAAGTAGGGAGATTATGAATATGCAAATAAGCACACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    864 ATCTCAGAGATATTTCCTTTTGTTATACACAATGTTAAGGCATTAAGTATAATAGTAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          684 igigiacacananaaacannacacirhaacccaraaanangnahahgahhangnahc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT
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Beta-Globulin Gene and Beta-Locus Control
Derivatives
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1666;
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Pred. No. 0.14;
                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc signal
LOCATION: 299.1148
OTHER INFORMATION: /note= "Intron 2"
FRATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/06661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1, LOCATION: 1502...1643

) OTHER INFORMATION: /note= "Exon I"

US-08-076-090-1
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                                                                                                                                                                                      ORGANISM: Homo sapiens
CELL TYPE: Beta-globin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1149..1370
OTHER INFORMATION: /note=
                                                                                          MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                       NAME/KEY: misc signal
LOCATION: 37..298
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 1371..1501
OTHER INFORMATION: /note=
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc signal LOCATION: 1502..1643
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TITLE OF INVENTION: BEC
TITLE OF INVENTION: DEX
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_signal
                      TYPE: nucleic acid
STRANDEDNESS: single
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OPERATING SYSTEM:
                                                                      linear
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Best Local Similarity
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LENGTH:
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nucleic acid
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               Chicago
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, LOCATION:
US-08-550-715-10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1151 TITCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TCTTAGGTTAAAAAACAAGTATATTACTAAACAATAAAAGAAAA 1330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           744 AATTGAAAATAAAAGAAAATAAAGTAGGGAGAGTTATGAATATGCAAATAAGCACACATAT 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       864 ATCTCAGAGATATTTCCTTTTGTTATACACAATGTTAAGGCATTAAGTATAATAGTAAAA 923
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APPLICANT: Bowie, Lemuel J.
TITLE OF INVENTION: Human '-Thalassemia Mutations as a Predictor of
TITLE OF INVENTION: Blood-Related Disorders
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 42.2; DB 5; Length 1666;
Pred. No. 0.14;
0; Mismatches 138; Indels 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PEATURE:
NAME/KEX: misc signal
LOCATION: 1371_1501
OTHER INFORMATION: /note= "Intron 1"
                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 37..298
OTHER INFORMATION: /note= "Exon III'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: misc signal
LOCATION: 11497.1370
OTHER INFORMATION: /note= "Exon II'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_signal
LOCATION: 1502..1643
CT-US94-06661-1
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Patent No. 5750345
FILING DATE: 10-JUN-1994
CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1666 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (Genomic)
HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                   ORGANISM: Homo Sapiens
CELL TYPE: Beta-globin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_signal
LOCATION: 299._1148
OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 2.5%;
Best Local Similarity 47.5%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                           misc_signal
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NAME/KEY:
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1151 TITCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT 1210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT 1270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1271 GGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAAACAATAAAAAGAAAAA 1330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1416 Arcreagagararirecrirreiraracacaarerraaggearraagrararaaraaaa 1357
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FILE REFERENCE: 1786.0017
CURRENT APPLICATION NUMBER: US/09/411,449
CURRENT PILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
PRIOR FILING DATE: 1999-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1536 AATTAAAAATAAAAGAAAATAAAGTAGGGAGATTATGAATATGCAAATAAGCACACATAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1091 ITTTTCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTATTGAAAATC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42.2% DB Lt. Length 2500;
Pred. No. 0.16;
0; Mismatches 3138; Indels 0
                                                  OMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CDS
join(687..778, 909..1131, 1982..2107)
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V: United States of America
60606-6402
                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/550,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/09411449
Patent No. 6524851
                                                                                                                                                                                                                                                                 FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: GASS, DAVIG A.
REGISTRATION NUMBER: 38,153
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 2.5%;
Best Local Similarity 47.5%;
Matches 125; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2500 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         single
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us-09-938-842a-3729.rni

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TYPE: DNA
ORGANISM: Homo sapiens
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US-09-411-449-2
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Best Local Similarity
                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: James E
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US-09-411-449-2/C
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SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1948 АТСТСАGAGATATTTCCTTTTGTTATACACAATGTTAAGGCATTAAGTATAGTAAAA 1889
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1091 TITITCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAAATTATTGAAAATC 1150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTAACCAGAATGAGTTTCTGATTT 1270
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GENERAL INFORMATION:

APPLICANT: James Ellis

TITLE OF INVENTION: HYBRID NUCLEIC ACID MOLECULES AND VECTORS INCLUDING

TITLE OF INVENTION: Deta-GLOBIN REGULATORY ELEMENTS

FILE REFERENCE: 17860017

CURRENT APPLICATION NUMBER: US/09/411,449

CURRENT AFFLICATION NUMBER: 2,246,005

PRIOR APPLICATION NUMBER: 2,246,005

PRIOR FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                 2068 AATTAAAATTAAAAGAAATTAAAGTAGGGAGATTÄTGAATATGCAAATAAGCACATAT
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2.5%; Score 42.2; DB 4; Length 3496;
Best Local Similarity 47.5%; Pred. No. 0.18;
Matches 125; Conservative 0; Mismatches 138; Indels 0
                                                                                                                                                       Length 3385;
                                                                                                                                                                                                        Indels
                                                                                                                                                     Score 42.2; DB 4;
Pred. No. 0.18;
0; Mismatches 138;
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                                                                                                                                                     ilarity 47.5%;
Conservative
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; SEQ_ID_NO_3
; LENGTH: 3385
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-411-449-3
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US-09-411-449-1
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Best Local Similarity
Matches 125; Conserv
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                                                                                                                                                                                                                                   TITLE OF INVENTION: DAMES LITTE OF INVENTION: DECA-GLOBIN REGULATORY ELEMENTS
TITLE OF INVENTION: Deca-GLOBIN REGULATORY ELEMENTS
TITLE OF INVENTION: Deca-GLOBIN REGULATORY ELEMENTS
TITLE OF INVENTION: Deca-GLOBIN REGULATORY ELEMENTS
CURRENT APPLICATION NUMBER: US/09/411,449
FRIOR APPLICATION NUMBER: 2,246,005
FRIOR PILING DATE: 1999-10-01
NUMBER OF SEQ ID NOS: 4
LENGTH: 3805
LENGTH: 3805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/09411449
Patent No. 6524851
Patent No. 6524851
APPLICANT: James Ellis
TITLE OF INVENTION: Beta-GLOBIN REGULATORY ELEMENTS
FILE REFERENCE: 1786001 NUMBER: US/09/411,449
CURRENT PILLING DATE: 1999-10-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 3805
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1999 ATTGCGGAGAAAAAAAAAAAA 1977
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PRIOR FILING DATE: 1998-10-01
NUMBER OF SEQ ID NOS: 4
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Best Local Similarity 47.5%;
Matches 125; Conservative
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Gaps ò

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Matches 125; Conservative
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                                                                             2659 igriciaciacaráriaaaacarracacrirraaccearaaarargrarargarrargrard
                                                                                                                         1151 TTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
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                                           TTTGCCTAACCAATAAAATTATTGAAATC
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  Mismatches 138; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Glazer, Peter M.
TITILE OF INVENTION: TREATMENT OF HEMOGLOBINOPATHIES
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30
RRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/09430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 42.2; DB 5;
Pred. No. 0.22;
                                                                                                                                                                                                                                                                                                                                                                                                              2419 ATTGCGGAGAGAAAAAAAAAGA 2397
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APPLICATION NUMBER: US 08/473,845.
FLIING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
                                         1091 TTTTCCATAAATTAAAGTAAATCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 7, Application PC/TUS9609430 GENERAL INFORMATION:
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ZIP: 20877

COMPUTER READBLE FORM:

MEDIUM TYPE: Floppy disk

TYPE: Floppy disk

Floppy disk

Floppy disk

Floppy disk

Floppy disk

Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FELECOMMUNICATION INFORMATION TELEPHONE: 301-527-2058
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MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 6060 base pair
  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      301-208-6997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POSITION IN GENOME:
CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaithersburg
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
STREET: 20
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  Matches 125;
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Sequence 2589, Application US/09107532A
Sequence 2589, Application US/09107532A
Patent No. 6583275
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Lynn A Doucette-Stamm and David Bush
APPLICANT: Lynn A Doucette-Stamm and David Bush
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
FITLE OF INVENTION: ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                            2916 ATCTCAGAGATATTTCCTTTTGTTATACACAATGTTAAGGCATTAAGTATAATAGTAAAA 2857
                                                                                                                3096 IGIGIACACATATTAAAACATTACACTTTAACCCATAAATATGTATAATGATTATGTATC 3037
                                                                                                                                                                           1151 TTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                                                                                                                                          3036 aattraaaataaaadaaatraaagaagattatdaatatgaaaataagcacacatat
                                                                                                                                                                                                                                                                                         1211 ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT
                                                                                                                                                                                                                                                                                                                                                    0; Mismatches 138; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OCERATING SYSTEM: «UDKNOWN»
SOTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
FRICK APPLICATION DATA:
APPLICATION NUMBER: 60/085,598
FILING DATE: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: JUNY 2, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
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REGISTRATION NUMBER: 40,489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2856 ATTGCGGAGAAGAAAAAAAGA 2834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1331 CATTTTGTGAAAAGAGAAATAAA 1353
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COMPUTER READABLE FORM:
MEDIUM TYPE: CD/ROM ISO9660
COMPUTER: PC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Waltham
STATE: Massachusetts
COUNTRY: USA
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SEQUENCE CHARACTERISTICS
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STRANDEDNESS: doub
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ADDRESSEE: GENOME
STREET: 100 Beaver
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us-09-938-842a-3729.rni

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ENGTH:
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                                                                                                              162 ATCTGAACAAGAAATCAAAGAGGCAGATGCAATCATTCTTGCAGTAGATAAAGAATGGA 221
                                                                                                                                                102 AAGAAATCTAAACCATCAAGCAAAATTTGGAAACAGAGGTGTAAAAACAGAAAATCAGTT
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                                                                                Gaps
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                                             Score 42; DB 4; Length 1440;
Pred. No. 0.15;
0; Mismatches 70; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
PELECOMMUNICATION INPORMATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                              1417 AAGTGATTTGTTCACGTGGTACAATCGGAATGGT 1450
                                                                                                                                                                                                                                                                                222 ATTGGACCGATTTGCCGGGAAAAAAGTAAAGCGT 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6239264artis Corporation
; SEQUENCE DESCRIPTION: SEQ ID NO: 2589:
US-09-107-532A-2589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-DEC-1997
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                                                                                                                                                                                                                                                                                                                                                                 Application US/08998416
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E: Research Triangle Park
E: No. 6239264th Carolina
TRY: USA
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IBM PC compatible
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                                                                                                                                                                                                                                                                                                                                                                                                                  .ippsen, Peter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Rebischung, Corin
FNTION: GENOMIC
                                               Query Match 2.5%;
Best Local Similarity 54.5%;
Matches 84; Conservative
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nucleic acid
EDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 27709
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Meigs, J. Timo
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PAG1241RP
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OPERATING SYSTEM:
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Length 837

DB 3;

2.4%; Score 39.6;

Query Match

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1331 CATTITIGIGAAAAGAGAAATAAAGTITTACTGGACCCCCATTGTACAGATGGTCCCATAATA 1390
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                                                                                                                                                                                                                                                                                       422
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                                                                                                         1151 TITCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGT
                                                                                                                                                                                                                                                                                       481 AAGTTAAATTTAATTAATAATAATTCTTATAAAAAGATTAAATAATAATAAATCAACAT
                                                                1091 TITITCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATTAT
  45.7%; Pred. No. 0.53;
iive 0; Mismatches 164; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F. G.
APPLICANT: FALKNER, F. G.
NUMBER OF SEQUENCES: 52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7218 base pairs
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Best Local Similarity 45.7 Matches 138; Conservative
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 435 PRIOR APPLICATION DATA:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Alexandria
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STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
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ATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTCTGATTTT 1270
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FILING DATE: 1997-08-22
                                                                                                                                                                                            1331 CATTTTGTGAAAGAGAATAAA 1353
                                                                                                                                                                                                                                    310 AAAAAATTAAAATCAAAAAA 332
                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/08991677A
Patent No. 6252135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome-
PATILE OF INVENTION: Jannaschii
TITLE OF INVENTION: Jannaschii
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EARLIER APPLICATION NUMBER: US 6
BARLIER FILING DATE: 1996-12-16
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Best Local Similarity 46.0%;
Matches 132; Conservative
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SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Pinus taeda
US-08-991-677-11
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                                                                                     2.4%; Score 39.6; DB 1; Length 7218; 10.9%; Pred. No. 1.1;
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GENERAL INFORMATION:
APPLICANT: FASE, NICCLAS JOSEPH
APPLICANT: REYMON, CHRISTOPHE DOMINIQUE
APPLICANT: REYMON, CHRISTOPHE DOMINIQUE
APPLICANT: REYMON; CHRISTOPHE DOMINIQUE
APPLICANT: REYMON; CHRISTOPHE DOMINIQUE
TITLE OF INVENTION: METHOD FOR EXPRESSING A DESIRED PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1; Length 731; 0.72;
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Pred. No. 0.72;
0; Mismatches 140; Indels
                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: THE WEBB LAW FIRM
STREET: 700 KOPPERS BUILDING, 436 SEVENTH AVENUE
                                                                                                                             24; Conservative 111; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: UNITED STATES OF AMERICA ZIP: 15219-1818
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" FLOPPY DISK
COMPUTER: Midwest Micro 486-50
OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 6.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/451,405A
FILING DATE: 26-MAY-1995
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Best Local Similarity 46.8%;
Matches 123; Conservative
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INFORMATION FOR SEQ ID NO: 2
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LENGTH: 731
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IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
IS-08-232-463-14
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                                                                                                       Best_Local Similarity
Matches 24; Conserv
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CLASSIFICATION:
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-08-451-405A-2
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STATE:
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                                                                                       Query Match
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Sequence of the Methanogenic Archaeon, Methanococc
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152 TTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTAGGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    794 TITTAAAATAATAGTGTTTAATTATTTTAGATTTTGAAATTTTTACTGTAATTTAACA
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APPLICANT: Carraway, Daniel T
APPLICANT: Smeltzer, Richard H
TILLE OF INVENTION: Production of Syringyl Lignin in Gymnosperms
FILE REPRENCE: 50617
CURRENT APPLICATION NUMBER: US/08/991,677A
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PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR FILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOSTWARE: Patentin version 3.1
SEQ ID NO
LENGTH: 1664976
TYPE: DNA
ORGANISM: Methanococcus jannaschii
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Query Match 2.3%; Score 39; DB 4; Length 1664976; Best Local Similarity 48.4%; Pred. No. 9.6; Matches 108; Conservative 0; Mismatches 115; Indels 0;

1025807 ATTTATCTATAATTTTTACTATTTCCTTTAGTTCTTTAAATACACTGGTGAGACATCAT 1025866

Search completed: February 2, 2004, 03:00:22
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1201 AAAGCTAGGTATTTCATTTGGAAGTGTACTAGTAACTAAGTACTAACCAGAATGAGT  1201 AAAGCTAGGTATTTCATTTGGAAGTGTACTAGTAACTAAC	Db 1501 AAAGGGTTGAATACTCACTTGTTTTCCTGCTCCTATATATA	-3729 9, Application No. US200400094 Marparion Expens, Joel Wargs, Joel Wargs, Toel Wargs, Toel Wargs, Toel Wargs, Toel Wargs, Strangel Wargs, Toel Wa	FRIOK FILING JUNE: 200-08-24  FRIOR APPLICATION NUMBER: US 60/364,647  FRIOR FILING DATE: 2001-01-16  FRIOR FILING DATE: 2001-06-22  FRIOR FILING DATE: 2010-06-22  NUMBER OF SEQ ID NOS: 5379  ERWINGER OF SEQ ID NOS: 5379  TYPE: DNA  CORANISM: Arabidopsis thaliana US-09-938-842A-3729	Ouery Match  Do. 08; Score 1677; DB 12; Length 1677;  Best Local Similarity 100.08; Pred. No. 0; Indels 0; Gape 0;  Matches 1677; Conservative 0; Mismatches 0; Indels 0; Gape 0;  Oy 1 GGTTAAGCGTTTACTTATGGTTTATATGGAAGAATATTGCCATGTTGGAATGG 60  Oy 61 TITTCAGATCATCAAGGCTCTACAAGTTGTTATATGCAAGAAATATTGCATTGTTGAATGG 60  Oy 61 TITTCAGATCATCAAGGCTCTACAATTGTTAAGGAATGGTTTGAGGCTTTTGTTA 120  Oy 121 GAAATTGTATATTGCAACAGTTAATTGTTAAGGAATGGTTTCAGGCTTTTGTTA 120  Oy 121 GAAATTGTATATTGCAACAGTTAAAAGGTTTCTAAGGAATGGTTTTGTTA 120
121 GAAATTGTGTTTATTGCAACAGGTAGACATAACCATAGACAGATGTATCTGAACAGA 180 121 GAAATTGTGTTTATTGCAACAGGTAGACATAACCATAGACAGATGTATCTGAACAGA 180 121 GAAATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACATGTATCTGAACAGA 180 181 TAAGCTTCTCTTATTGTCTAAAGAAATGGACCGATACGAATAAAACAACATAAAACAT 240 181 TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAAACAACATTAAAGAT 240 241 TAAATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAATGAAAAGT 300 241 TAAATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAATGAAAAGT 300 241 TAAATGGTTTGTAAGAAATACTACAATTATTGTGAAAATTTTGATGCTGGCG 360 301 AAAAACATCGGAATCCAAAACCTCAAATTTACCAATCAGCCCAAATTATTGATGCTGGCG 360 301 AAAAACATCGGAATCCAAAAACTTACCAATCAGCCCCAAATTATTGATGCTGGCG 360 301 AAAAACATCGGAATCCAAAAATTTACCAATCAGCCTGGGAAAATTATTATTATTATCGCGG 360 361 TAATGAATGGTAGGTAGGCAAAAAGTTGGTGGGAAAATTACAACATTATC 420	CCTCTGTGGTGGACCCGAATCTGTAATCGGAAAGGTGGAACCCACTTGGTTTAACTTTT CCTCTGTGGTGGACCCGAATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTT AAGCCTAAAAGGTTACTACTGTTGACCGGTTTATAATTTGGTGTTTAATTCTAATCCC AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTGTTTAATTCTAATCCC AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTTTAATTCTAATCCC GGATCCGTTTGTTAGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTTGAGTG GGATCCGTTTGTTTGTTTTGT	601 GGTAGGGAATGGTGGGGTCGAATAGTTGGGCCTAGCCTCAACAATGTGGAAG 660  [11	AACTTACAATCATTTCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATAT 900  AACTTACAATCATTTCGATTACTTTGATCTGATTTCTAGTTCGGTTTGTATGTTTAATAT 900  CCGGATTGTACAAGTACACAAGTACATAAGTATGCGTATATGTATG	961 AAAGACGACGATAGGAGGATTTTGGAATCCTGGAAAGAATTATTCCATAGACACTA 1020 1021 ATTAGCTTTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGTCCAACCCCAAGTATG 1080 1021 ATTAGCTTTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCAAGTATG 1080 1021 ATTAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCCCAAGTATG 1080 1081 GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAATT 1140 1081 GGCTTACAGCTTTTTCCATAAAATTAAAGTTAAATTTTTTTT

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1201 AAAGCTAGGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGAGTAGTAGTAAGAAGTTTTGAAGCTTTTCTTAGGTTAAAAAAAGAAGTAGTTTTGTTTTTTTT	Oy 1321 AAAGAAAACATTTGGAAAAAAAAAAAAAAATTACTGGACCCCATGTACAAATGA 13 Db 1321 AAAGAAAACATTTGGAAAAGAAAAAAAAAAAAAAAAAAA	1501 AAAGCGTTGAATACTATTCTCACCTTGATTTTCCTGCTCCTATATATTTT  1501 AAAGCGTTGAATACTATTCTCACTTGTTTTCCTGCTCCTATATATA	Db 1561 ACATTTAGTAATCTCCTTGGACGTGTAAAACGATTAAAAACGATTTTTTCCCATTGTATCC 16  OY 1621 GCTTTTAACAACTCTCGTCGTCTCCACGTCCGTTTTTTTCTCTCAGCTATATTTTA 1677  Db 1621 GCTTTTAACAACTCTCGTCGTCATCTCCACGTCCGTTTTCTCTCAGCTATATTTTA 1677  1621 GCTTTTAACAACTCTCGTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTTTA 1677	3,7 3,7 108 1. B	APPLICANT: CLAU, T.  APPLICANT: Han, B.  APPLICANT: Wang, X.  APPLICANT: Cooper, Bret  TITLE OF INVENTION: Promoters for regulation of plant expression  FILE REFERENCE: 1360.001US1  CURRENT PRPLICANTON NUMBER: US/09/887,576  CTRODENT PILITON NUMBER: US/09/887,576	PPLICATION NUMB LLING DATE: 200 PPLICATION NUMB PLICATION NUMB PPLICATION NUMB LLING DATE: 200 DE SEQ ID NOS:	73 2000 1. Arabidopsis thaliana 6-73 1. Similarity 47.1%; Pred. No. 0.067,	Matches 161; Conservative 0; Mismatches 181; Indels 0; Gaps  QY 1075 AGTATGGGCTTACAGCTTTTCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATA 11  Db 1019 ATTAGGTTCGTATCTTTAACTAAAAAAAAAAAAACTATATGAATGA	DD 959 AGAAATTGAAGTACGAAACAGGTCCTAAAACTGTTCTTATTTGGTATGATATCAT 90
	241 TAAATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAGTGAAAGT 300 241 TAAATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGTTAGTGATAGAAAGT 300 301 AAAAACATCGGAATCCAAAACCTCAAATTTACCAATCAGCCCAAATTATTGTGTGCTGGCG 360 301 AAAAACATCGGAATCCAAAACCTCAAATTACCAATCAGCCCAAATTATTGATGCTGGCG 360 301 AAAAACATCGGAATCCAAAACCTCAAATTACCAATCAGCCGAAATTATTGATGCTGGCG 360	361 TAAIGAATGGTATGGTAGGCAAAAGTTGGTGGCTGCGAAAATTACAACATAATC 420 361 TAATGAATGGTATGGTAGGCAAAAGTTGGTGGCTGCGAAAATTACAACATAATC 420 421 CCTCTGTGGTGGACCCGAATCTGTAATCGGAAAAGTTGGTTG	481 AAGCCTAAAAGGTTACTACCGGTTTGACCGGTTTATAATTTGGTGTTTAATTCTAATCCC 540 481 AAGCCTAAAAGGTTACTGCGGTTTGACCGGTTTATAATTTGGTGTTTAATTCTAATCCC 540 541 GGATCCGTTTGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTGATTTTTGAGTG 600 541 GGATCCGTTTGTTTATTTAATCTCAAGGCCACGTTATCGCCAATATTTGATTTTTGAGTG 600 541 GGATCCGTTTGTTTAATCTCAAGGCCACGTTATCGCCAATATTTGAATTTTGAGTG 600	601 GGTAGGGAATGGTGGGGCCGAATAGTTGGGCCTCAACAATGTGTGGAACTGAAG 660  601 GGTAGGGAATGGTGGGGCTCGAATAGTTGGGCCTCAACAATGTGTGTG			961 AAAGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGATTATTCCATAGACACTA 1020	1081 GGCTTACAGCTTTTTCCATAAATTAAAGTAATTTTTTTTT	aaagctaggtapttcapttgggagtgtactagtaactagtaagtaagtaactaa

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NAME/KEY: unsure
LOCATION: (379615)
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     1315 AACAATAAAAGAAAAACATTTTGTGAAAAAGAAATAAAAGTTTACTGGACCCCATTGTAC 1374
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                                     AAGTGTTTTTTTTTTTTTTTTTTTTTTTTAAGAACCGAAACTTGATCAGTTATTA 780
                                                                                                                                                                                      779 GACAAGCGAAGCTACCCTTTGTGTTTGTTGACGATCCTATAATAAAGTTTTTCACGGAAC
                                                                           ATGAGTTTCTGATTTTTGGATTTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTA
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APPLICANT: Wang, You'zhen
APPLICANT: Steinman, Kathleen
APPLICANT: Steinman, Kathleen
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS
TITLE OF INVENTION: THERAPY OF BREAST CANCER
TILLE OF INVENTION: THERAPY OF BREAST CANCER
CURRENT APPLICATION NUMBER: US/10/199,846
CURRENT FILING DATE: 2002-07-18
PRIOR REPELICATION NUMBER: 60/306,220
PRIOR FILING DATE: 2001-07-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.0%; Score 49.6; DB 15; Length 858; 42.1%; Pred. No. 0.2; 1ve 0; Mismatches 162; Indels 0;
                                                                                                                                                                                                                           1375 AGATGGTCCCATAATAATACTGATAGAAGATAGAGCAATGGA 1416
                                                                                                                                                                                                                                                             719 eccendadeeriaarcecarderadaadaaadardeerdaa 678
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SETTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 7035
LENGTH: 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCATION: 509, 513, 517, 526, 488, 17HER INFORMATION: D = A, I, C. or G = AME/KRV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ON: 253, 259, 276, 279, 281, ON: 320, 321, 327, 338, 349, INFORMATION: n = A,T,C or G
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ION: 722, 735, 739, 750, 75
ION: 722, 735, 739, 750, 75
ION: 832, 833, 838, 842, 84
INFORMATION: n = A,T,C or
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Best Local Similarity 42.1%
Matches 118; Conservative
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1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTA 1207

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APPLICANT: Epigenomics AG
TITLE OF INVENTION: Disgnose von bedeutenden genetischen Parametern innerhalb des MHC
TITLE REPERENCE: B01/1208/W0
CURRENT APPLICATION NUMBER: US/10/312,841
CURRENT FILING DAIE: 2002-12-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               genetischen Parametern innerhalb des MHC
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                                                                                                     1268 TITGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAAA 1327
                                               262 AAGNTTTTANNANATTTTNNNANNNTAAATTTTTTNNTAAANANTAAANNCNTTTTTT 203
                                                                                                                                                     1096 CCATAAAATTAAAAGTAAATCTTTTTTGCCTAACCAATAAAAATTATTGAAAATCTTTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1216 ATTIGGGAGIGIACTAGIAACTAGIAAGIACTAACCAGAATGAGIITCIGATITIGGAIT
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OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                          1328 AAACATTTTGTGAAAAGAGAATAAAGTTTACTGGACCCC 1367
                                                                                                                                                                                                                                                          Score 49.2; DB 13;
Pred. No. 19;
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                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
APPLICANT: Epidenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden gen
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
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Best Local Similarity 49.2%
Matches 129, Conservative
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PPLICANT: Wang, Xun
PPLICANT: Wang, Xun
PPLICANT: Zhu, Tong
TPLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING:
TILE OF INVENTION: SAME, AND METHODS OF USE
ILE REPERENCE: SCRIP1300-3
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TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND
                                                      1347
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                                                                                                     350 ATAAATAAAGGAGGATAATATTACTAAATAGCCAAAAAAACAACGTAAAATAGCAGA 291
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  410 ATTAGCAACTAGCTAGTAATAAGTGTTTTTAGAAGTATTTTACAAAGTATTTTACAAGGGTTCTATC 351
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                                                                                                                                                                                                                                                                                                                230 AAAACAATCCTTCGTTTGCAAGTTCAACAGTAGGCGAGACACTT
                                                      1288 TTAGGTTAAAAAACAAGTATATTACTAAAACAATAAAAGAAAAACATT
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Pred, No. 1; Seconds
0; Mismatches 112; Indels
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PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-06-22
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 338
LENGTH: 2958
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US20020137139A1
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Best Local Similarity 50.7%?
Matches 115; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                        2587593 TTATCCCCATATTTAAAATAAAAACTAAAATCAAAAATCATTTCTCAAAAATAA 2587534
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                                                                                                  FEATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
                                                                                                                                                                                                                                                                                       Length 3673778;
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                                                                                                                                                                                                                                                                                                                                     0; Mismatches 170; Indels
                                                                                                                                                                                                                                                                                       DB 13;
21;
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                                                                                                                                                                                                                                                                                       Score 49;
Pred. No.
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FILING DATE: 2001-01-16
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CATION NUMBER: US 60/300,111
IG DATE: 2001-06-22
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US20020160378A1
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ORGANISM: Arabidopsis thaliana
                                              TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 50.7%;
Matches 115; Conservative
                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 47.0%;
Matches 151; Conservative
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                                                                                                                                                                            NAME/KEY: unsure
LOCATION: (3294164)
JS-10-312-841-1
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                        3673778
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SEQ ID NO 1
                                                                                                                                                      FEATURE
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APPLICANT: BERLIN, Kurt
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
TITLE OF INVENTION: Dy Means of Assessing the Methylation Status of Genes Associated
TITLE OF INVENTION: With DNA TRANSCRIPTION
FILE REFERENCE: 5013.1009
                                                                                                                                                                                                                                                                                                                           1084 TIACAGCITITICCATAAAATIAAAGTAAATCITITITIGCCIAACCAATAAAATTAIT 1143
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ORGANISM: Artificial Sequence
FRATURE:
OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
FRATURE:
                                                                                                                                                                                                                   Length 7047;
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Pred. No. 3.4;
0; Mismatches 146; Indels
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; LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)
US-10-240-453-38
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PRIOR APPLICATION NUMBER: DE 10019058.8
PRIOR FILING DATE: 2000-04-06
PRIOR PLING DATE: 2000-04-06
PRIOR PELING DATE: 2000-04-07
PRIOR PELING DATE: 2000-04-07
PRIOR FILING DATE: 2000-04-07
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-09-01
NUMBER OF SEQ ID NOS: 350
LENGTH: 17848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/EP01/03973
PRIOR FILING DATE: 2001-04
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Best Local Similarity 49.77
Matches 145; Conservative
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Best Local Similarity
                                                                                                               ; NAME/KEY: unsure
; LOCATION: (182)
US-10-240-453-259
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FILE REFERENCE: 5013.109
CURRENT APPLICATION NUMBER: US/10/240,453
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: PCT/EP01/03973.
PRIOR APPLICATION NUMBER: 0001-04-06
PRIOR FILING DATE: 2001-04-06
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 516;
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                                                                                                                                                                                                                                               NAME/KEY: unsure

: LOCATION: (76).(90)

OTHER INFORMATION: unsure at all n locations

: OTHER INFORMATION: Clone ID: 25-LIB3057-018-Q1-K1-G1

US-09-960-352-5785
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Pred. No. 0.78;
0; Mismatches 179;
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PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: DE 10032529.7
PRIOR FILING DATE: 2000-06-30
PRIOR FILING DATE: 2000-06-01
PRIOR FILING DATE: 2000-09-01
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Best Local Similarity 46.2%;
Matches 154; Conservative
             FILE REFERENCE: 16511.006/37.
CURRENT APPLICATION NUMBER: 1
CURRENT FILING DATE: 2001-0.
NUMBER OF SEQ ID NOS: 15112
SEQ ID NO 5785
LENGTH: 516
                                                                                                                                                                                                     ORGANISM: Bos taurus
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9927 ATAAAATAATAACTAAAATTAAAAAAAAAATATATTAACATTTTTAATTT
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TITLE OF INVENTION: Identification and Mapping of Sing)
TITLE OF INVENTION: Polymorphisms in the Human Genome
FURE REFERENCE: 108827,129
FURE REFERENCE: 108827,129
CURRENT APPLICATION NUMBER: US/10/027,632
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PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FASUSED for Windows Version 4,0
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PRIOR FILING DATE: 2000-07-12
PRIOR APPLICATION NUMBER: US 60/198,676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 233686, Application US/10027632
Publication No. US20030204075A9
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Best Local Similarity 62.3%;
Matches 71; Conservative
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 6
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APPLICATION NUMBER: US 6
FILING DATE: 1999-11-23
APPLICATION NUMBER: US 6
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                                                                                                                                                                                                                                                                                              9867 ТАТАААААААТТААААСАТАТТТТАААТТААСАДАААТААТСТААТ<del>ААЛААААДАААА</del>
                                                                                                                                                                                                                                                                                                                                                                                                                                               1328 AAACATTTTGTGAAAAGAAAAAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCATA 1387
                                                                                              .0047 AACTTAAAAAAAACAATTTTAAAAATATTAAAAATAAAAACCTAATTAAATATAAAA 9988
                                                                                                                                             1148 ATCTTTCCAACCATAGAAAAGTTAAATTTGATCAGCGATGGAAATTTTTGTACAAAGCTA 1207
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TITLE OF INVENTION: Diagnosis of Diseases Associated with Gene Regulation
TITLE SEPERENCE: 5013.1003
CURRENT APPLICATION UNBER: US/10/239,676
CURRENT FILING DATE: 2002-09-24
                                                                                                                                                                                               1208 GGTATTTCATTTGGGAGTGTACTAGTAACTAGTAAGTACTAACCAGAATGAGTTTTCTGAT
                                                                                                                                                                                                                                                                                                                                                TITGGATTITGAAGCTTTTCTTAGGTTAAAAACAAGTATATTACTAAACAATAAAAGAA
                                               1088 AGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTTGCCTAACCAATAAAAATTATTGAAA
  Gaps
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2.8%; Score 46.4; DB 15; Length
Best Local Similarity 45.6%; Pred. No. 5.5;
Matches 164; Conservative 0; Mismatches 196; Indels
  0; Mismatches 196; Indels
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LOCATION: (6075, 8510, 8516, 8680, 9019, 15666)
10-239-676-28
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PAROR APPLICATION NUMBER: PCT/EP01/03968

DE 10019058 8

DE 10019173.8
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APPLICANT: PIEPENBROCK, Christian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 2001-04-06
2000-04-06
Matches 164; Conservative
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EQ ID NO 28
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AAACATTTTGTGAAAAAGAGAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCCATA
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TITLE OF INVENTION: Identification and Mapping of Single Nuclectide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT FILING DATE: 2002-04-30
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1325 GAAAAACATTTTGTGAAAAAGAGAATAAAGTTTACTGGACCCCATTGTACAGATGGTCCC 1384
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NUMBER OF SEQ ID NOS: 325720
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 233686
LENGTH: 616
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2000-06-15
JMBER: US 60/216,820
2000-07-07
                                                                                                                                                                               FILING DATE: 1999-11-23
APPLICATION NUMBER: US 60/156,358
FILING DATE: 1999-09-28
APPLICATION NUMBER: US 60/146,002
FILING DATE: 1999-08-09
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                         7-12
US 60/198,676
                                                                                                    NG DATE: 2000-03-29
ICATION NUMBER: US 60/185,218
NG DATE: 2000-02-24
ICATION NUMBER: US 60/167,363
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US 60/218,006
                                                                                 SICATION NUMBER: US 60/193,483
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Best Local Similarity 62.3
Matches 71; Conservative
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1179 TCAGCGATGGAAATTTTTTGTACAAAGCTAGGTATTTCATTTGGGAGTGTACTAGTAACTA 1238
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                                                                                                                                                                                                                                                                                                                     Score 45; DB 13; Length 502;
Pred. No. 1.8;
                                    Indels
                                    0; Mismatches 120;
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   2.7%;
                  Best Local Similarity Matches 117; Conserva
     Query Match
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	9	AX506339 Sequence	AY113981	AY056214	9680	3579	53.79	5623	3874	2955	2217	384	328	3493	1344	3604 9604	5043	7400	3178	5649	D87261 O	AE004632	AP003513	3569	2074	AL392174	AP005848	1807	1804	4000	1672	AY150488	Arosovie Arabidops Arabidops	AK118679 Arabidop			1.000 000 000 000 000 000 000 000 000 00			de la companya de la		Embryophyta; Tracheophyta; dons; core eudicots; decese: Trachidons;		ic plants containing
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	SUMMER I	AX506339	AY113981	AY056214	AC003680	AK118579	AY086379	AB025623	AY058874	ATF1P2	BX322174	AY056384	AC013289	AF165924 BT008493	AY081344	AC079131	BT006043			AB026649	D87261	APU04632 CNS07YPE	AP003513	AP003569	AYU/2620 AF412074	ATF8L15	AP006175	AF411807	AB071804	AC120539	AP004672	AY150488	AY080776	AK118679	ALIGNMENT	 -	-	3	576	(thale or		ie; Str ophyta;	3	Wang, s of pl
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NLMKKKKRKRPSNSEYIDISDAVSASSGLAPIATTTTQPPQALASSTVAQQLLPQGMY
PMWAIPSNAMIPTVGAFFLIPQIAGPSNQPQLLAFFAAAASPSSYVAAVQQASTWARP
PPLQVVPSSGFVSVSDVSGSNLSRATSVMAPSSSSGVTTGSSSSIATTHTLRDFSL
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lepkaepvmpsfsmslappsstgpplkrastkdrhtkvegrgrrirmpatcaarifql
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.

[Dases 1 to 1071]
Lam, B., Southwick, A., Warlin-Neumann, G., Nguyen, M., Miranda, M.,
Chung, M. K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H.,
Bilm, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R. W.
Direct Submission
Submitted (17-APR-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                     901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA
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Arabidopsis thaliana putative PCF2-like DNA binding protein
(At2945680; F17K2.21) mRNA, complete cds.
AF370606
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(protein_id="AAK43925.1"
|db_xref="GI:13877695"
                                                                                                                                                                                                                                                                                                           1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e-mail for correspondence: arab@sequence.stanford.edu
This clone was isolated by RT-PCR.
_Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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|mol_type="mRNNA"
| Azref="Laxon:3702"
|chromosome="II"
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ilarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
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/gene="At2g45680; F17K2.21"
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/gene="At2g45680; F17K2.21"
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Arabidopsis thaliana (thale cress)
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; rosida; eurosida II; Brassicales; Brassicaceae; Arabidopsis.

1 [bases: 1 to 102]

Yamada,K. Banh,J., Chan,M.M., Chang,C.H., Chang,E., Dale,J.M., Deng,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Quach,H.L., Tang,C., Toriuni,M., Wu,H.C., Yamamurary,Y., Yu,G., Bowser,L., Carrinci,P., Chen,H., Cheuk,R., Hayashizaki,Y., Telhida,J., Jones,T., Kamiya,A., Karlin-Neumann,G., Kawai,J., Kim,C., Lam,B., Lin,J., Miranda,M., Narusaka,M., Nguyen,M., Palm,C.J., Sakurai,T., Satou,M., Seki,M., Shinn,P., Southwick,A., Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A.
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product="putative PCP2 DNA binding protein"
protein ld="AAM45059:1"
db xref="G1:21261085"
translation="WATIQKLEEVAGKDQTLRAVDLTIINGVRNVETSRPPQVNPTVS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (16-MAY-2002) Plant Gene Expression Center, 800 Buchanan
Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yamada, K. (SSP/PGEC) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Theologis, A. (SSP / FGEC) contributed equally to this work as PIS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yamada, K., Banh, J., Chan, M.M., Chang, C.H., Chang, E., Dale, J.M., Deng, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Tornumi, M., Wul, R.C., Yamamura, Y., Yu, G., Bowser, L., Carainci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T. Satou, M., Seker, J. Southwick, A., Shinozaki, K., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the DUNI (ORF) clones using the RAFL CDNAs: Yamada, K., Banh, J., Chan, M. M., Chang, C. H., Chang, E., Dale, J. M., Dengy, J. M., Goldemith, A.D., Lee, J. M., Onodera, C. S., Quach, H. L., Tarag, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Bowser, L., Chen, H., Cheuk, K., Jones, T., Karlın-Neumann, G., Kim, C., Lam, B., Lin, J., Miranda, M., Nguyen, M., Palm, C. J., Southwick, A., Davis, R.W., Ecker, J. R. and Theologis, A.
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The RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA; 'RIKEN Arabidopsis Full-Lendh cDNA'); Seki,M., Narusaka,M., Ishida, Satcu,M., Ramiya,A., Sakuraa,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
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'mol_type="mRNA"
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ecotype: Columbia"
1, 1102
                                                                                                                                                                   Arabidopsis thaliana (thale cress)
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chromosome="2"
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100.0%; Score 1071;
Best Local Similarity 100.0%; Pred. No. 0;
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ramada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee-J.W., Quach, H.L., Torium, M., Yu, G., Bowser, L., Corninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Tishida, J., Bowser, L., Lin, J., Miranda, M., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Batin-Neumann, G., Kawai, J., Kim, C., Lam, B., Barton, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K., Sakurai, T., Arabidopsis Full Length cDNA Clones
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Arabidopsis thallana putative PCF2 DNA binding protein (At2g45680)
mRNA, complete cds.
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Location/Qualifiers
1. .1660
                                                                                    901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA 960
841 GTIGITCCAAGCAGCGGCTITGTATCCGTTTCAGACGTTAGCGGTTCGAATTTTATCAAGA 900
                                                                                                                                                                             901 GCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACAACGGTAGTTCATCGTCA 960
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Spermatophyta, Magnoliophyta, eudicotyledons, Core eudicots,
rosids, eurosids II; Brassicales, Brassicaceae; Arabidopsis.
1 (bases 1 to 1660)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and amotation of the RAFL CDNAS: Yanada,K., Banh,J., Bann,J., Guch,H. L., Tang,C.C., Toriumi,M., Yanamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Kim,C. Koesema, B., Lam,B., Liin,J., Meyers,M.C., Miranda,M., Nguyen,M., Ecker,J.R. Southhick,A., Tracy,S.E., Davis,R.W.
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this work. Shinozaki,K. (RIKEN GSC) and Theologis,A. (SSF/PGEC)
contributed equally to this work as PIs.
                                                                                                                                                                                                                                                                  961 ATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                           1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATGAACACTGA 1071
1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA 1071
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Arabidopsis thaliana
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
1 (bases 1 to 91854)
110, X, Kaul,S.; Town,C.D., Benito,M.-I.; Creasy,T.H., Haas,B.J.,
Mu,D., Maiti,R. Romning,C.M., Koo'H., Fujil,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome 2 BAC F17KZ genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            1002
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(Losses 1 to 91854)

Town.C.D. and Kaul, S.

Direct Submission
Submitted (27-FEB-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598396.

Address all correspondence to:at@tigr.org
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The orientation of the sequence is from SP6 to T7 end of the BAC
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                                            CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG
                                                                   CAAGCTCTGGCATCATCTGACTGTGGCTCACTTCTGCCGCAAGGAATGTATCCGATG
                                                                                                                                TGGCCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAA
                                                                                                                                                                          763 resecratrocarcaaacecaarcaarcecacesceaecerrerrerrerrearrecada
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                                                                                                                                                                                                                                                                                                                                                /product="putative PCF2 DNA binding protein"
/protein id="AAL07063.1"
/b_xref="G1:15810351"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRELGHKSDGETIRWLLENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTTNADSDMGE
MIKKKKRESBSBYIDISDAVSASSGLAPIATTTIQPPQALASSTVAQQILPOGMY
PMWAIPSNAMIPTVGAFFLIPQIAGPSNQPOLLAFPAAAASPSSYVAVQQASTWARP
PPLQVVPSSGFVSVSDVSGSNLSRATSVMAPSSSSGVTTGSSSSIATTTTHTLRDFSL
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                                                                          /clone="RAFL07-08-P04 (R10678)"
/hote="This clone is in a modified pBluescript vector
(FLC-1) as a BamH1/XhoI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCCGTTTCAGCTTCCTCCGGTTTAGCTCCACACGACGACGACGACGACCCCCG
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llarity 100.0%; Pred. No. 0;
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organism "Arabidopsis
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                  mol_type="mRNA"
db_xref="taxon:3702"
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/gene="At2g45680"
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0022. 4215,4582. 4712,4769. 4864,4948. 5188,5352. 5374,
5506. 5585,5670. 5980))
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TEGKLYBLCIKKHRFISOVTDKRVSGSDLQALCEBAAMMPIRELGANILTIQANKVLN
FSVSQINVEVCLSLKGLINRCVHVTGKISTI"
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GPRICLGKDPAYRQMKIVSMALLHFPRFKMADENSKVYYKRMLTLHVDGGLHLCAIPR
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YTLAEIDGRSKRKEREKKYWEAKKOKKOKKGKTEDTLERNFPKHEDIRFOKUVQAPLKLA
VYPKARKSTLSASQERLRLQAIDAYRSRKGWTARPGVPIPAVMMQ"
                                                                                                                                                                                                                                                                                                                   SSEKEKVRSYREKISNWQNQVSERLQALGVGMSENKRTVAYPSSASVSSTASRYRKTL
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ADLLGHGIFAVDGEKWROORKLSSFEFSTRVLRDFSCSVFRNASKLVGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RRFLVESEKDPENMUDKYLRDIILNPMIAGKDTTAALLSWFLYMLCKNPLVQEKIVQE
IRDVTPSHEKTTDVNGFVESINEBALDEMHYLHAALSETLRLYPPVPVDMRCAENDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MEILTSIAITVATTIFIVLCFTIYLMIRIFTGKSRNDKRYAPVH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VSEFALSGKAFDAQDLLMRCTLDSIFKVGFGVELKCLDGFSKEGQEFMEAFDEGNVAT
                                                                                                                                                                                                                                                                                                                                                   OKTPVARGGVATPRNPKDAAASPKPVKESGNVYDDKLVEMINTTIVDRSPSVKWDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SSRFIDPLWKLKWPFNIGSQSKLKKSIATIDKFVYSLITTKRKELAKEQNTVVREDI
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Ceres:35578"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(8412. .9632)
/gene="At2g45520"
/note="synonym: F17K2.5; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="synonym: F17K2.4"
oin(<6429. .6950,7026. .7310,7386. .7724,7806. .8006,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1100. ... 2238)

1101. ... 2238)

Gene="At2g45510"

1101. (429. .6950,7026. .7310,7386. .7724,7806. .8006,

1100. .8288)

Gene="At2g45510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (join(*8412. .8678,8768. .8903,8987. .9120,
9289. .9356,9459. .>9632))
/gene="At2g45520"
/gene="At2g45520"
9289. .9356,9459. .9612))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   codon_start=1
product="putative_cytochrome_P450"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            product="expressed protein"
protein_id="AAC06155.1"
db_xref="G1:2979546"
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'product="expressed protein"
'protein_id="AAC06154.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein_id="AAC06153.1"
db_xref="G1:2979544"
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/rpt_family="(CA)n"
complement(9578. .9632)
/rpt_family="(GA)n"
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gene="At2g45530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            822. .10798
gene="At2g45530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          429. .8288
gene="At2g45510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ceres:82<u>2</u>0"
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http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GilmmerM, see Mihaela Pertea all GeneMark/), GlimmerA (a variant http://www.tigr.org/softlab/glimmerm.htm/glimmerm.html, and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/cdb/cdb/glishtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wistl.edu/eddy/tRNAscan-SE (Sean Eddy, http://genome.wistl.edu/eddy/tRNAscan-SE (Sean Eddy, http://genome.washington.edu/RN/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RN/Repeatmasker.html).
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complement(join(<3414. .3616,3639. .3825,3916. .3965,
0092. .4215,4882. .4712,4769. .4864,4948. .5188,5352. .5374,
5506. .5555,5670. .>5980))
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CHMHRGMKKKHPVDTTNSHENAGFSPLTVETAVRSVVPCKDGDDQKHSVSVMGITLPR
/SDEKSTSSCGTDTTITDTALRGEDDDEBYLSLFSPGV"
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(GGELYGVLKQNGHLTEQQAATYIASLSQALAYCHGKCVIHRDIKPENLLLDHEGRLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IADFGWSVQSSNKRKTWGGTLDYLAPEWYENRDHDYAVDNWTLGILCYBFLYGNPFFE
AESQKDTFKRILKIDLSFPUTPNVSEEAKNLISQLLVKDPSKRLSIEKIMQHPWIVKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ranslation="MSKKSTESDAGNTEKQWSLADFEIGRPLGKGKFGRVYLAREAKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tränslation="DESKPSVQKFFPEVSDKCLEAAKFSSNRKNDIIARSREWKNMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                omplement(1. .1281)
note="overlap with BAC clone F4L23 (AC002387:1. .1281)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: F17K2.2; contains a protein kinase domain
rofile (PDCC00100)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     omplement(join(<1002. .112,1208. .1280,1366. .1580,
1655. .1750,1886. .2128,2260. .>2388))
gene="At2g45490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (join(1002. .1112,1208. .1280,1366. .1580,
655. .1750,1886. .2128,2260. .2388))
gene="At2g45490"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roduct="putative protein kinase"
rotein_id="AAC06151.1"
b_xref="G1:2979542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               organism="Arabidopsis thaliana"
mol type="genomic DNA"
cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="hypothetical protein"
protein id="AAF18607.2"
db_xref="G1:20197053"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="synonym: F17K2.27"
oin(<57. .242,335. :>747)
gene="At2g45480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  oin(57. .242,335. .747)
gene="At2g45480"
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/gene="At2g45500"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           db xref="taxon:3702"
chromosome="2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene="At2g45480"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      map="CIC02E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   clone="F17K2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
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74111 ATGGCTGGCTGCTGAATCAGCTCAGTTATTAGCTTTTCCCGGCGGCGGCTGCTTTAGAA 74351 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCACAATGGCTTGAACCACCTCCTTTACAA 74351 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCAATGGCTTAGACCACCTCCTTTACAA 841 GTTGTTCCAAGCAGCGCTTTTGTATCCGTTTCCAGACGTTAGCGGTTCGAATTTATCAAGA 74291 GTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCCAGACGTTAGCGGTTCGAATTTATCAAGA 74291 GTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCCAGACGTTAGCGGTTCGAATTTATCAAGA 7421 GCGACGTCGGTTATGGCTTCCAAGCTCAAGCGTTAGCGGTTCGAATTTATCAAGA 901 GCGACGTCGGTTATGGCTTCCAAGCTCAAGCGTTAACAGACCGGTTAGTTCATCGTCA 74231 GCGACGTCAACAACAACAACAACACACACACAGCATAGTTCATCGTCAA 74111 ATTGCAACAACAACAACAACACACACACACACACACACAC	BT008779 MRNA linear PLN 13-JUN Arabidopsis thaliana At5g51910 mRNA, complete cds. PLN 13-JUN 200879 BT00879. G1:31711723 BT00879. FLI CDNA. STORE ARABIDOPSIS thaliana (thale cress) Starbidopsis thaliana (thale cress) Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheoph Spermatophyta, Magnoliophyta, eudicotyiedons; core eudicots.	rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis I thases I to 882]  Xim, C. J., Chen, H., Cheuk, R., Shinn, P., Bowser, L., Carninci, Dale, J.M., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lini, J., Mixanda, M., Narusaka, M., Nguyen, M., Onodera, C. S., Palm, C. J., Quach, H.L. Sakurai, T., Sacou, M., Seki, M., Southwick, A., Toriumi, M., Wu, H.C., Yamada, K., Yu, G., Shinozaki, K., Davis, R.W., Theolo Mrabidopsis ORF clones		NYEAN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA : 'RIKEN Arabidopsis Pull Length CDNA'): Seki,M., Narusaka,M., Ishida Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J.; Hayashizaki,Y. and Shinozaki,K.  The Salk, Stanford, PGBC (SSP) Consortium members constructed sequenced the pUNI (ORF) clones using the RAFL CDNAS: Kim.C.J. Chen,H., Cheuk,R., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin, Miranda,M., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Yamada,Yu,G., Davis,R.W., Theologis,A., and Ecker,J.R.
음	RESULT 6 BT008779. LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	REFERENCE AUTHORS TITLE JOHNAL	AUTHORS AUTHORS TITLE JOURNAL	COMMENT
/db_xref="G1:2979545" /translation="MOSSSSGGDDLEKQQQQQXDKSPQKQSESANESNHLTIVVCN GDSRELVGOTPPEREVSLENGCSHDCRVCLQDKEFVLIELGCORGGLAX4HRS CIDAWFRIKGSNQCEICQVVANVTPPETQPTVNYWWRIDPSYRQERERGGFSPLW VARAVQRAEANNFSNIAYPPAL"  VARAVQRAEANNFSNIAYPPAL"  9980. 10007  /rpt family="(CAG)n"  complement(10833. 25573) /gene="Atzg45540" /note="synonym: F172."  complement(join(<10833. 11272,11438. 11560,11636. 12378,	ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 60	181 GCTCCACCGTCTTCGACGACCACCATTGAAGACCTTCGACTAAAGACCGTCACGCGTCACGCGTCACGCGTCACCGGGGGGGG	361 AACGTGAGGGGGATTATAGCCGCCACGGGGAAAGGATTCGGTGGTTGGT	74551 AATCTGATGAAGAAGGAAGCTTAGCCCTTCTAACAGTGAGTATATAGACATAAGGAAC 74592  541 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGACCAACCTCCG 600  74591 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGACCAACCTCCG 600  74591 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGAATGTATCCGATG 600  74531 CAAGCTCTGGCATCATCCACTGTGGCTCAACTTCTTCGCCGCAAGGAATGTATCCGATG 600  74531 CAAGCTCTGGCATCATCCACTGTGGCTCAACCTTCTGCCGCAAGGAATGTATCCGATG 74472  90 G61 TGGGCTATTCCACCAAAAGATTCCGAAGGTTTCTTTCTTT

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AY086379
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Arabidopsis thaliana At5g51910 mRNA for unknown protein, complete
                                                                                                                                                                                                                                                                                                                                                            PVKTKPAPKR PTSKDRHTKVEGRGRRIRMPAGCAARVFQLTRELGHKSDGETIRWLLE
                                                                                                                                                                                                                                                                                                                                                                               RAEPAI IEATGTUVPAIAVSVNGTLKIPTSSPVLNDGGRDGDGDLIKKRRKRNCTSD
                                                                                                                                                                                                                                                                                                                                                                                                   FVDVNDSCHSSVTSGLAPITASNYGVNILAVVNTQGFVPFWPMGMGTAFVTGGPPQMGQ
WWAIPTVATAPFLNVGARPVSSYVSNASDAEAAEMETSGGGTTQPLRDFSLEIYDKREL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryoca; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  141 GACTAAACCGGCTCCGAAGAGACCGACTTCTAAAGACCGTCACACGAAAGTAGAAGGACG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201 AGGTCGGAGGATCCGAATGCCGGCGGTTGCGCTCGCGTCGTTTCAATTGACCCGTGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  315 GTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           375 GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      261 actrodricacaaarccdacddadaaacdaracddricarrifddaacdadcrdaacdddd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               321 GATAATTGAAGCAACCGGAACCGGAACTGTACCGGCTATTGCTGTATCGGTTAACGGAAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Seki, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakaima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.
Arabidopsis thaliana full-length oDNA.
Published Only in Database (2002)
2 (bases I to 1046)
2 (kases I to 1046)
2 (kases I to 1046)
2 (kase, M., Iida, K., Satou, M., Sakurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Narusaka, M., Carninci, P.,
              Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) equally to this work as PIs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 882;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.7%; Score 157.8; DB 8; 75.9%; Pred. No. 1.4e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62;
                                                                                       'organism="Arabidopsis thaliana"
mol_type="mRNA"
db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Mismatches 62
                                                                                                                                                                                    51
                                                                                                                                                                                    'note="This clone is in pUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                            204 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FLI CDNA, CAP trapper.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                      rotein_id="AAP68218.1"
b_xref="GI:31711724"
                                                                                                                                                                                                                                             note="unknown protein"
this work. Shing... contributed equally to this ... Location/Qualifiers
                                                                                                                                                                                                                                                                                   t="At5g51910"
                                                                                                                                                                                                      ecotype: Columbia"
1. .882
                                                                                                                                                                                                                                                                                                                                                                                                                                                            250 g
                                                                                                                                                                                                                                                                                                                                                                                                                                       QFLGGSGNSSPSSCHET"
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AK118579
AK118579.1 G1:26452181
                                                                                                                                                  'chromosome="5"
                                                                                                                                                                    clone="U60996"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 75.9
Matches 195; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                          236
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VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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JOURNAL
REFERENCE
AUTHORS
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AK118579
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                                                    FEATURES
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Direct Cubmission

Submitted (15-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences
Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Nokohama, Kanagawa
230-0045, Japan (E-mail:meskingso:riken.go.jp,
UKL:http://pfgweb.gsc.riken.go.jp, Tel:81-45-503-9625,
Pax:81-45-503-9866)
An Arabidopsis full-length cDNA library was constructed essentially
as reported previously (Seki et al. (1998) Plant J. 18:707-720;
Seki et al. (2002) Science 296:141-145), cDNA claeved with BamHI
and XhoI was ligated to modified lambda FLC-1-E vector (Carninci et
al. (2001) Genomics 77:79-30) digested with BamHI and SalI.
This clone is in a modified pBluescript vector.
Please visit our web site (http://pfgweb.gsc.riken.go.jp/) for
further details.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /tränslation="mesnhegnalqvidgyttmthisdpnpyttkegmmimkgedgylg
pvktkpapkrptskdrhtkvegrgrrirmfagcaarvrqitrelghksdgetirwlis
raepalieatgtgtvpalavsvngtlkiptsspvlndgrbdddbilkkrrkknustsd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
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Arabidopsis thaliana clone 247645 mRNA, complete sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FVDVNDSCHSSVTSGLAPITASNYGVNILINVNTQGFVPFWPMGMGTAFVTGGFDQMGQ
MWAIPTVATAPFLNVGARPVSSYVSNASDABABABTSGGGTTQPLRDFSLXDKREL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          187 GACTAAACCGGCTCCGAAGAGACCGACTTCTAAAGACCGTCACACGAAAGTAGAAGGACG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 314
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                307 ACTIGGICACAAAICCGACGGAGAAACGAIACGGIGGITATIGGAACGAGCIGAACCGGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   375 GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       14.7%; Score 157.8; DB 8; Length 1046; 75.9%; Pred. No. 1.4e-36; 1ndels 0; Mismatches 62; Indels 0;
Kawai, J., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Arabidopsis thaliana"
/mol type="mRNA"
/cultivar="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="common name: thale cress"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene="At5g51910/MJM18 6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'gene="At5g51910/MJM18_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'clone="RAFL19-81-E01"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'db xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAC43179
/db_xref="GI:26452187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             location/Qualifiers
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FLI_CDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . .1046
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us-09-938-842a-1034.rge

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All Submitted (102-APR-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research; 1532-3, Yana, Kisarazu, Chiba 202-0812, Japan (E-mail:ynakamuskazusa.or.]p.
Tel.81-438-52-3955, Fax:81-438-52-3934)
Address for correspondence: Kaos@kazusa.or.jp s c.ne, please see http://www.kazusa.or.jp/kaos/691-bin/agd_Graph.cgi?c=MJM18
Genes with aimilarity to proceins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity to proceins in the databases are described in 'product' or 'note' qualifiers. Genes that have no significant protein similarity are described as 'unknown protein.'
The software programs used to predict genes include: Grail (Informatics Group, Oak Ridge National Laboratory).
Http://compbio.ornl.gov/Grail-13/), http://compbio.ornl.gov/Grail-13/), http://comptio.ornl.gov/Grail-13/), http://comptio.ornl.gov/Grail-13/), http://comptio.ornl.gov/Grail-13/), http://comptio.ornl.gov/Grail-13/), http://comptio.ornl.gov/Grail-13/), http://cremlinl.zool.iastate.edu/cgi-bin/sp.cgi)
Bennark http://www.das at predicted by krankean-SE (Sean Eddy, Washington University, School of America and ynot be the entire insert of this clone. It may be shorter because we remove over lank because and includent seinmissione
                                                                                                                                                                                                                                                                                                                                                                                             AB025623
Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone:MJM18.
AB025623 BA000015
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The 5' clone is MIO24 and the 3' clone is MSG15.
Location/Qualifiers
   378 ACTIGGICACAAAICCGACGGAGAAACGAIAGGGIGGIIATIGGAACGAGCIGAACCGGC 437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tracheophyta;
                                                                                                                              438 GATAATTGAAGCAACCGGAACCGGAACTGTACCGGCTATTGCTGTATCGGTTAACGGAAC 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asamizu, E., Kotani, H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               375 GATTATAGCCGCCACGGGTACGGGACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC
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kharyota, Viridiplantae, Streptophyta, Embryophyta, Tracheol
Spermatophyta, Magnoliophyta, endicotyledons; core endicots,
rosids; eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Structural analysis of Arabidopsis thaliana chromosome 5. X. Squence factures of the regions of 3,076,755 bp covered by P1 and TAC clones
DNA Res: 7 (1), 31-63 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       note="CDS is reported in Acc# AB010074
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organism="Arabidopsis thaliana"
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/product="MADS box transcri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana (thale cress)
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AB025623/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                 DEFINITION
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VERSION
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MEDLINE
PUBMED
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Submitted (11-MAX-2002) Ceres, Inc, 3007 Malibu Canyon Road, Malibu, CA 90265, USA

This clone sequence is one of 5,000 Ceres full-length cDMAs made available to TIGR and Genbank. The following quality assessment of this set was done by comparison with known proteins: two percent of the clones are estimated to be 5'-truncated; less than one percent are 3'-truncated; approximately two percent alternative splice variants, including unspliced introns and spliced exons; one percent may contain premature stop codons; five percent may have frame shifts in a coding region. A sequence is considered to be 5'-truncated if it lacks the translation initiation start (ATG). A sequence is considered to be 3'-truncated if it lacks the C-terminal end of the encoded protein. Please note that these CDNA sequences are derived from the Ws or Laker cootypes and therefore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /trānslation="MLMKQEDGYLQPVKTKPAPKRPTSKDRHTKVEGRGRRIRMPAGC
AARVFQLTRELGHKSDGETIRWLLERAEPAIIEATGTGTVPAIAVSVNGTLKIPTSSP
VLNDGGRDGFODLMKKRRRRNCTSDFVDVNDSCHSSVTSGLAPITASNYGVNILNVNT
QGFVPFWPMGMGTAYVTGPDCMGQMWAIPTVATAPFLNVGARPVSSYVSNASDAEAE
METGGGGTTQPLRELEIYDKRELELPLGFGGSGNSSPSSCHET"
225 c 293 g 32.t
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Eukaryota, Viridiplantaes, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnollophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        258 GACTAAACCGGCTCCGAAGAGAGCGGACTTCTAAAGACCGTCACAGAAAGTAGAAGGACG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGCTAGGATTTTTCAATTAACTCGAGA 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       318 AGGTCGGAGGATCCGAATGCCGGCGGGTTGCGCTCCGGGTCTTTCAATTGACCCGTGA 377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    315 GTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        may contain polymorphisms when compared to sequences from Coll-0. Genset carried out the library production and sequencing of the full-length clones. Ceres, Inc. carried out the clustering of the 5' sequences, selection of clones, and sequence assembly.
                                                                                                                                                                                                                                                                                                                                                                                                 (bases 1 to 1156)
.ver,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         rover, V., Troukhan, M., Alexandrov, N., Lu, Y.-P., Flavell, R. and sldmann, K.
                                                                                                                                                                                     Haas, B.J., Volfovsky, N., Town, C.D., Troukhan, M., Alexandrov, N. Feldmann, K.A., Flavell, R.B., White, O. and Salzberg, S.L. Full-length messenger RNA sequences greatly improve genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                    Brover,V., Troukhan,M., Alexandrov,N., Lu,Y
Sedhann,K.
Full-Length cDNA from Arabidopsis thaliana
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
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/clone="247645"
                                                                                                                                                                                                                                                                                                                Genome Biol. 3 (6), RESEARCH0029 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein_id="AAM64446.1"
db_xref="GI:21592496"
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product="unknown"
                                                                                                                                                              (bases 1 to 1156)
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Best Local Simi.
Matches 195; (
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TTASALTWFFWFLSENPLVVTKIRQEIDMNLPRSCSGQERPSCDPMEYLAKDDESCMG
RRCIRIQAREMDFRDRRVSIQCRSRICHGKQRAMVQMKIVAVEILQNYDIKVANGQKF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="Mapskglifamifavlalvkpsbaaldahvydgscpaaekiile
vRNatlydpkvparllemffhdcfirgcdasilldstrsnqaekdgppnisvrsfyv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SYLKWHDLFTVENCITSDESKAFVKTAESLGFTHQGSRCPAYGEAYRDNHRISWNDPV
LADTLWQSGLSNLFTDIKIRRKVAVGLNPNIRFYRYSAGQHFGRHIDESADLEDGNRT
YYTLLIYLSGNSTKSKSKSSSSKTNDSSSAEPLVGGETVFYGSRNSIVAEVVEGMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPPTFNVSQLIQSFAARGLSVKDNVTLSGGHTIGFSHCSSFESRLQNFSKFHDIDFSM
NYAFAQTLKKKKCPRTSNRGKNAGTVLDSTSSVFDNVYYKQILSGKGVFGSDQALLGDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ranslation="MYRHVKPRFSWKLQSWIGVGMEKKMIEAGAIFDRVCGKYISARR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aivesosgrlheysssomekiidrygkfsnáfyvaerpoveryloelkmeidrmykti
ollevhhrkliggglidscsyteloeidtoiekslriyrsrkaelyadolkklikekere
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       canslation="MVRGKIEIKKIENVTSRQVTFSKRRSGLFKKAHELSVLCDAQVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                translation="MNLTNLISLNLILNPPOKPRNAKMGDNGESIKWPKIKLKSNLNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EDAKRKLEKACPRTVSCADVIAIAARDVVTLSGGPYWSVLKGRKDGTISRANETRNL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(8854: 9420,9536: 9724,9814: 10026))
/note="gene_id:MJM18.4"
/codon_starE=1
                                                                                                                                                                                                            complement (431, 492)
/product="MADS box transcription factor-like protein"
/note="CDS is reported in Acc# AB010074
/number=3
/number=3
  complement (22]. 320)
/product=MADS box transcription factor-like protein"
/note==CDS is reported in Acc# AB010074
gene_id:MJM18.1"
                                                                                                                                                                                                                                                                                                                                                                                       /evidence=not_experimental
complement (1636/11817)
/product="MADS box transcription factor-like protein<sup>8</sup>
/product="NADS reported in Acc# AB010074
gene_id:MJM18.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |oin(7086, .7247,7585; .7832,8043; .8262,8344; .8466)
|note="gene_id:MJM18.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /evidence=not experimental
complement(jnn(3326. 3412,3636. 3701,3811. 3852.
3943. . 4042/4175. 4236,4360: 4444,5433. .5614))
/note="gene_id:MJM18.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LINERKRILEEVINMHSSKGNTEGGHRTKHSSEVETDLFIGLPVTRL"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      evidence=not_experimental
product="MADG box transcription factor=like";
protein_id="BAA97222.1"
db_xref="GI:8809681"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(Join(11372, 11638,11684, 12145))
/note="contains similarity to cytochrome P450
gene_id:MJM18.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LFHIHGDKCMLHEGRNVSKGVKYVFRSDVVFA"
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product="peroxidase"
protein_id="BAA97224:1"
db_xref="GI:8809683"
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protein_id="BAA97225.1"
db_xref="GI.8809684"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'codon_start=1
'evidence=not_experimental'
'protein_id="BAA97223:1"
'db_xref="G1:8809682"
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                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="Mesnhegnalgyidgyttwitledpnpktkpgmmlmkqedgyldprkrepapkrptskorhikkerpredering pvkrkepapkrptskorhikkerpredering prkrepapkrptskorhikkerprederingide prespalifateringidgypalaysvygytistringspyptwithgyldprederingidgyrvatapfilmygarpytgypomygwalpyratygystowad maaiptvatapfilmygarpytgyspomygmanityvatapfilmygarpytgyspomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytgypomygmytetinygarpytetinygarpytetinygarpytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgypytetingidgy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  254
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Kin, C. J. Chen, H., Cheuk, R., Neyers, M.C., Shinn, P., Banh, J.,
Bowser, L., Carning, P., Chang, B., Dale, J. W., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin Neumann, G.,
Kawai, J., Lam, B., Lee, J.W., Lin, J., Miranda, M., Narusaka, M.,
Ngyen, M., Chodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T.,
Satou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,
Theologis, A. and Ecker, J.R.
Theologis, A. and Ecker, J.R.
Arabidopsis ORF clones
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       375 GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Kim C.J., Chen.H., Cheuk.R., Meyers, M.C., Shinn, P., Banh, J.,

Kim C.J., Carning, P., Chang, R., Dale, J.M., Goldsmith, A.D.,

Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,

Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narueska, M.,

Nguyen, M., Onodera, C.S., Palm, C.J., Onach, H. L., Sakurai, T.,

Satol, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C.,

Yamada, K., Yamanura, Y. Yu, G., Yu, S., Shinozaki, K., Davis, R.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13136 GACTAAACCGGCTCCGAAGAGCCGTCTAAAGACCGTCACACGAAAGTAGAAGGACG
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                                                                                                  DNA binding protein PCF1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 157.8; DB 8; Length 16203; Pred. No. 2.1e-36;
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                                                                                                        similarity
                                                                                                                                                                                                                 /codon start=1
/evidence=not_experimental
/protein_id="BAA97226.1"
/db_xref="G1:8809685"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
RPDTSLILKOMCHGFKVKINKRCSS"
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a 2906 c 2744 g
                                                    complement (12395.
/note="contains si
gene_id:MJM18.6"
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Best Local Similarity 75.9%;
Matches 195; Conservative
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us-09-938-842a-1034.rge

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Shinn, P., Chen, H., Cheuk, R., Kim, C.J., Koesema, E., Meyers, M.C.,
Banh, J., Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D.,
Hayashizaki, Y., Ishida, J., Jiang, P.X., Jones, T., Kamiya, A.K.
Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X.
Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J.,
Pham, P.K., Quach, H.L., Sakurai, T., Sarcu, M., Seki, M., Southwick, A.,
Tang, C.C., Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S.,
Arabidopsis cDNA clones
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protein 1a="AAL24251.1"
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                                                                                                                         AY058874 11near PLN 03-NOV-2001
Arabidopsis thallana AT3947620/F1P2_170 mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryoča, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II. Brassicales, Brassicaceae, Arabidopsis.
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Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                clone="RAFL09-09-C11 (R14172)
                                                                                                                                                                                                                                      FLI CDNA.
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
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GKHDPDDHHQQQPSPSSSSSLFBLLHQQQQLSQSQPQSQSQKSQPQTXQSKELLQYQBES
AVVJAKKPPLKRAZYCRHTKVDGRGRRIRMPLCAARVFQLTRELGHKSDGETIEML
LQQAEPSVIAATGTGTIPANFTSLNISLRSSGSSMSLPSHFRSAASTFSPNNIFSPAM
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'gene="FIP2.10"

join(113. .430,519. .1199,1277. .1420,1498. .1788,1869. .2054,

join(113. .2209,2378. .2437,2672. .2734,3123. .3214,3344. .3440,

1135. .2209,2378. .4392,4519. .4659,4737. .4904,5138. .5322,

1916. .5584,5671. .5759,5842. .6067,6228. .6302.6413. .6526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATFIP2 101154 bp DNA linear PLN 30-NOV-1999 AAAbidopsis thaliana DNA chromosome 3, BAC clone F1P2.
AL132955.1 GI:6434210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 translation="MHIKEICLEGFKSYATRTVVPGFDPHFNAITGLNGSGKSNILDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JTRQIVVGGKNKYLINGKLAQPNQVQNLFHSVQLNVNNPHFLIMQGRITKVLNMKPME
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ONANGNAELDRLKRFCVAFEYVOAEKIRDNSIHVVEEMKIKMTGIDEQTDKTQGEISE
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Information on performance of analysis and a more detailed
annotation of this entry and other sequences of chromosomes 3, 4
and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CFVLGITNLQQVRAANLQELVYKQGQAGITRATVSVTFDNSERNRSPLGHEDHSEIT
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EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

Eucher Submission

Submitted (30-NOV-1999) MIPS, at the Max-Planck-Institut fuer

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Hemcke@mips.biochem.mpg.de.mayer@mips.biochem.mpg.de Project

Coordinator: Marcel Salanoubat and Francis Quetier, Groupement
d'Interet Public, Centre National de Sequencage - GENOSCOPE; 2 rue

Gaston, Cremieux, BP191, 91006 Evry Cedex, France;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   note="strong similarity to CHROMOSOME ASSEMBLY PROTBIN" CAP-E - Xenopus laevis, SWISSPROT:XCPE_XENLA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Choisne, N., Robert, C., Brottier, P., Wincker, P., Cattolico, L., Artiguenave, F., Saurin, W., Weissenbach, J., Mewes, H.W., Lemcke, K., Mayer, K.F.X., Quetier, F. and Salanoubat, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana (thale crees)
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyt
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; nagnoliophyta; eudicotyledons; core eudicots; cosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
249 AGGAAGAGGAGAAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAAC
                                                                                                                                                     474 GCGAGAGCTAGGTCATAAATCCGACGGTGAGACAATAGAGTGGCTTCTTCAACAAGCTGA
                                                                                                                                                                                                             369 GCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCCGCCATCGCCATGTCGGTTAA
                                                                                                                                                                                                                                                                534 ACCATCTGTAATCGCCGCCACCGGAACCATCCCGGCGAATTTCACTTCTTTAAA
                                               414 cigaadaddaddadaahaaddandccedcerrarigrecadcradgerrirrrcageraac
                                                                                                     309 TCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGA
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mol type="genomic DNA"

variev="y="columbia"

db_xref="taxon:3702"

/chromosome="3"
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RDPVKNFDRSKYKGYVAKLIKYNDRSSMTALEVTAGGKLFNVIVDTEDTGKQLLQKGD
LRRAYTI FDLNKIOSHLVPPRVQQATVGKGNAELALSLUGYSBELKKAMEYVFGSTFV
CKTYDAAKEVAFNREIRTPSVTLEGDVYGPGGLLTGGSRKGGGDLIRQLHDLABAETK
PRAGOKSLSTIFANIKELQPLQTKFTDMKAQLELKKAMSIFIKRAEQNSHHIAGDAV
KKLEEEVEENRSQIKEKEGLYKSCADTVSTLEKSIKOHDKNREGRLKDLAGAA
lekoi kaltoareasmggevkalsdkvdslsnevtrelski tnmedtloggeeknaekm
                                                                                                                                                                                                                                                                                             KVNODFGSIPSTLLPGTMSKLEPPEGGFFLDGLEVRVAFGDVWKQSLSELSGGGRSLLA
ALSLILALLLFKPAPIYILDEVDAALDLSHTQNIGRMIKSHFPHSQFIVVSLKEGMFS
                                              EKCLEDOLRDAKI SVGTAETELKOLNTKI SHCEKELKEKKSOLMSKODEAVAVENELD
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MEMEHKNCSVKVDKLVEKHTMI I SEKRI FGNGCI DYDFESRDPHKAREELERLOTDOS
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                                                                 ARIONDVESVKRAFDSLPYKEGOMEALEKDRESELEIGHRLKDKVHBLSAQLANVOFT)
                                                                                                                                                                                                                                                                         SLEKRVNKKVTAMPEKAEDEYNALMTKKNIIETDKSKIKKVIEBLDEKKKETLKVTWV
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1869. .2054
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                                                                                                                                                                                                                                                                                                                                                                        113. .430
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/number=1
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gene="F1P2.10"
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/gene="F1P2.10"
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|ene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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/gene="F1P2.10"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        31. .518
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gene="F1P2.10"
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gene="P1P2.10"
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gene="F1P2.10"
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Submitted (31-MAR-2003) Clarke J.H., John Innes Centre, Colney Lane, Norwich, NR4-700, UK
AT denotes an activation ted dissociation transposon within a single line; ET an enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a mis-expression enhancer trap dissociation transposon, MT a mis-expressor mutator transposon, 3 denotes a sequence derived from the 3'end of the transposon. 5 denotes a sequence derived from the 5'end of the transposon BESRC GARNet, ATIS project
On-line seed stock requests: http://masc.nott.ac.uk/ NASC stock
                                                                                                                                                      72666 GGCAGCTAAAAAGCCACCGTTGAAACGAGCGTCGACGAAAGACCGACACACGAAAGTAGA 72725
                                                                                                                                                                                                                                 72786 GCGAGAGCTAGGTCATAAATCCGACGGTGAGACAATAGAGTGGCTTCTTCAACAAGCTGA 72845
                                                                                                                                                                                                                                                                                                                                                                                        72846 ACCATCTGTAATCGCCGCCCGGAACCGGAACAATCCCGGCGAATTTCACTTTTAAA 72905
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                                                                                                                                                                                                                                                                        368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BX322174 10-JUN-2003 Axabidopsis thaliana transposon insertion STS SM_3.35210, sequence
                                                                                                                                                                                                                                                                                                                                                   369 GCCGGCCATTATAGCCGCCACGGCTACGGGAACGGTTCCCCGCCATCGCCATGTCGGTTAA 428
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Arabidopsis thaliana (thale cress).
Arabidopsis thaliana
Bukarayopiyta, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                'note="Derived from superpool 26.24 NASC code Unknown"
                                                                                                                   GTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGTCACCAAAGGTTGA
                                                                                                                                                                                           249 AGGAAGAGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAAC
                                                                                                                                                                                                                                                                          309 TCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGA
                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Clarke, J.H., Bowles, B., Carter, J.; Hart, D., McCullagh, B., Murphy, G., Langham, S., LeGrys, C., Jones, J.D.G. and Bevan, M.
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                                      tch 12.0%; Score 129; DB 8; Length 101154; al Similarity 71.0%; Pred. No. 1.9e-27; 171; Conservative 0; Mismatches 70; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mol type="genomic DNA"
variety="Columbia-0 NASC stock code N1092"
db_xref="taxon:3702"
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139 c 87 g 83 t
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73.1%;
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      homolog"
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Best Local Similarity
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BX322174
LOCUS
DEFINITION
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PROTEIN 4 PRECURSOR (LHCI TYPEIII CAB-4) - Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        product = "CHLOROPHYLL A-B BINDING PROTEIN 4 PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement join (6970, 7100,7191, 7457,7537, 7685,913, 8121))
gene="F1P2.20"
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3916. .4032
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gene="F1P2.10"
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gene="F1P2.10"
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Jene="F1P2.10"
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jene="F1P2.10"
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jene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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gene="F1P2.10"
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RESULT 14 AY081706 LOCUS

ORGANISM

VERSION KEYWORDS SOURCE

REFERENCE AUTHORS

TITLE JOURNAL REFERENCE AUTHORS

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1 (bases 1 to 1440).
Cheuk, R., Chen, H., Kim, C.J., Koesma, B., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Dale, J.W., Goldsmith, A.D., Hayashizaki, Y., Ishida, J., Jiam, B., Lee, J.M., Lin, J., Lau, S.K., Miranda, M., Marusaka, M., Ngurang, P. K., Din, J., Lau, S.K., Miranda, M., Quach, H.L., Saturan, C.J., Pham, P.K., Ouach, H.L., Saturai, T., Satu, M., Seki, M., Southwick, A., Tang, C.C., Traindi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K., Arabidopsis cDNA clones
Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VRPKNESHSSSSSSQLLDHNOMGNYLVQSTAGSLPTSQSPATAPFWSSGDNTQNLWA
FNINPHHSGVVAGDVYNPNSGGSSGGSGGVHLMNFAAPIALFSGQPLASGYGGGGGGG
EHSHYGVLAALNAAYRPVAETGNHNNNQONRDGDHHNHQEDGSTSHHS"
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VIAATGTGTIPANPTSLNISLRSSRSSLSAAHLRTTPSSYYFHSPHQSMTHHLQHQHQ
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Makaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 978;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 ATCCCGACGACGACGACGCTGATTCTGATATGGGTGAAATC 484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 124.6; DB 8;
Pred. No. 2.2e-26;
0; Mismatches 99;
                                                                                                                                                                                                                                                                                                  /note="This clone is in pUNI 51
ecotype: Columbia"
ed equally to this work as PIs
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      product="At1g69690/T6C23_11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FLI CDNA.
Arabidopsis thaliana (thale cress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="unknown protein"
                                                                                                                              organism="Arabidopsis"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'protein_id="AALB7359...
'db_xref="G1:19547991"
                                                                                                                                                                    /mol_type="mRNA"
/db_xref="taxon:3702"
/chromosome="1"
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                                                                                                                                                                                                                                                                                              clone="U14268"
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Best Local Similarity 65.0%;
Matches 184; Conservative
                contributed equally
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DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AY056384
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AUTHORS
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                                                          FEATURES
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Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Arabidopsis thaliana (thale cress)

Busaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

E (beuk, R., Chen, H., Kim, C. J., Meyers, M.C., Banh, J., Bowser, L., Carninci, P., Chang, E., Dale, J., M., Goldsmith, A.D., Haysshizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Lam, B., Lee, J.M., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Onodera, C.S., Palm, C.J., Quach, H.L., Sakurai, T., Sakou, M., Seki, M., Southwick, A., Tang, C.C., Toriumi, M., Wu, H.C., Yamada, K., Theologis, A., Andrews, A., Yu, G., Yan, S., Shinozaki, K., Davis, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, A., Andrews, R.W., Theologis, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andrews, A., Andre
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAS (RAFL CDNA): 'RIKEN trabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                     248
                                                                                                                                                                                292
                                                                                                                                                                                                                                                            308
                                                                                                                                                                                                                                                                                                                                        293 CGGAAGAGGAGGAGAATAAGGATGCCGGCGTTATGTGCAGCTAGGGGTTTTTCAGCTAAC 352
                                                                                                                                                                                                                                                                                                                                                                                                                        368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                353 GCGAGAGCTAGGTCATAAATCCGACGGTGAGACAATAGAGTGGCTTCTTCAACAAGCTGA 412
                                                                                                                                                                                                                                                            249 AGGAAGAGGAGAAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAAC
                                                                                                                                                                                                                                                                                                                                                                                                                        GTTGGAGAACGCTGA
                                                                                                189 GTCTTCGACAGGACCACCATTGAAGAGCCTTCGACTAAAGACCGTCACACGAAGGTTGA
                                                                                                                                                                                GOCAGCTAAAAAGCCACCGTTGAAACGAGCGTCGACGAAAGACCGACACACGAAAGTAGA
                     Gaps
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Arabidopsis thaliana At1g69690/T6C23_11 mRNA, complete cds.
AY081706
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                         59; Indels
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                     0; Mismatches
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Unpublished
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                         160; Conservative
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PLN 03-OCT-2001

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COMMENT

TITLE JOURNAL

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk)

Theologis, A., and Ecker, J.R.

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Cheuk, R., Chen, H., Kim, C.J., Koesema, E., Meyers, M.C., Banh, J.,
Bowser, L., Carninci, P., Dale, J.M., Goldsmith, A.D., Hayashizaki, Y.,
Ishida, J., Jiang, P.K., Jones, T., Kamiya, A., Karlin-Nemmann, G.,
Kawai, J., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M.,
Narusaka, M., Nguyen, M., Onodera, C.S., Pallm, C.J., Pham, P.K.,
Quach, H.L., Sakurai, T., Satou, M., Seki, M., Sout, W., Yang, C.C.,
Toriumi, M., Yamada, K., Yamamura, Y., Yu, G., Yu, S., Shinozaki, K.,
Davis, R.W., Theologis, A. and Bcker, J.R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The Salk, Stanford, PGEC (SSP) Consortium members carried out the sequencing and annotation of the RAFL cDNAs: Chenk, R., Chen, H., Kim, C.J., Koesem, E., Meyers, M.C., Shinn, P., Banh, J. Bowser, L., Dale, J.M., Goldsmith, A.D., Jiang, P.X., Jones, T., Karlin-Neumann, G., Lam, B., Lee, J.M., Lin, J., Liu, S.X., Miranda, M., Nguyen, M., Ondera, C.S., Palm, C.J., Paman, P.K., Yamannra, R. Nguyen, M., Tang, C.C., Toriumi, M., Yamada, K., Yamannra, Y., Yu, G., Yu, S., Davis, R.W., Theologis, A., and Ecker, J.R.
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|db_xref="GI:15912213"
|translation="MDPDPDHNHRPNPPLQLLDSSTSSSSTSLAIISTTSEPNSEPKK
                                                                                                                                                                                                                                                                                                            Direct Submission Submitted (10-SEP-2001) Salk Institute Genomic Analysis Laboratory (SIGNAL), Plant Biology Laboratory, The Salk Institute for Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VI AATGTGTI PANFTSLNI SLRSGRSSLSAAHLRTTPSSYY FHSPHQSMTHHLQHQHQ
VRPKNESHSSSSSSQLLDHNQMGNYLVQSTAGSLPTSQSPATAPFWSSGDNTQNLWA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPPKRTSTKDRHTKVEGRGRRIRMPAMCAARVFQLTRELGHKSDGETIEWLLQQAEPA
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EHSHYGVLAALNAAYRPVAETGNHNNNQQNRDGDHHHNHQBDGSTSHHS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL CDNAs (RAFL CDNA: 'RIKEN Arabidopsis Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262 AGGATACGGATGCCTGCCACGTGTGCGCTAGGATTTTTCAATTAACTCGAGAGTTAGGT 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          322 CACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        262 CACAAATCCGACGGTGAAACTATTGAGTGGCTACTCCAACAAGCAGAACCAGCGGTTATA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 11.6%; Score 124.6; DB 8; Length 1440; Best Local Similarity 65.0%; Pred. No. 2.3e-26; Matches 184; Conservative 0; Mismatches 99; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          organism="Arabidopsis thaliana"
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product="At1g69690/T6C23_11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="unknown protein"
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/db_xref="taxon:3702"
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses and

Claim 144; SEQ ID NO 1034; 577pp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising:

(a) contacting nucleic acid representative of expressed polynucleotides in the plant cell with an array or probes representative of the plant cell genome; and

(b) detecting a profile of expressed polynucleotides in the plant cell characteristic of a stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants with increased tolerance to abloic stress. The present sequence is that of an Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 1071 BP; 287 A; 288 C; 256 G; 240 T; 0 other;

Gaps . DB 24; Length 1071; 0; Indels Mismatches Score 1071; Pred. No. 0; .. 100.0%; Query Match Best Local Similarity 100. Matches 1071, Conservative

9 1 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 1 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAAGGCAAAGATCAAACTCTAAGAGCCGTT

TCGGTTAACGGAACCTTAAAATCCCGACGACGACGAACGCTGATTCTGATATGGGTGAA 480 AATCTGATGAAGAAGAAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGAC 540 TCGGTTAACGGAACCTTAAAAATCCCGACGACGACGAACGCTGATTCTGATATGGGTGAA AATCTGATGAAGAAGAAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGAC 421 421 481 481

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TGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTT 661

961: ATTGCAACAACGACGACGACGACGACGAGAGACTTCTCCCTAGAGATATACGAGAAAAAA 1020 900 960 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAA 840 661 TGGGCTATTCCATCAAACGCAATGATTCCGACGTCGGAGCTTTCTTCTTCATTCCACAA 721 Arcecreerecatecatactecreagnianiacinaringecececececece GITGITCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGGTTCGAATTTATCAAGA 8 881 GTTGTTCCAAGCAGCGTTTCTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGA GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA 901 GCGACGTCGGTTATGGGTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA 961 ATTGCAACAACAACGCCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA 1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCAGGGTCATCGAACCACTGA 1071 1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCAGGGTCATCGAACCACTGA 1071 781 781 841 721 001 යු ද P. 8 ි පු કે g

ABX61156 standard; DNA; 460 ABX61156; RESULT 2 ABX61156/c

RESULT

(first entry) 26-FEB-2003

Arabidopsis thaliana polynucleotide #502

Thale cress; gene; de; genetic manipulation; plant; blosynthesis; genetic modification; environmental stress; disease resistance; fungicide; insecticide; stress tolerance

Arabidopsis thallana: US2002142319-A1.

03-OCT-2002.

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07-AUG-2001; 2001US-0924035 13-AUG-1999; 99US-148784P 11-AUG-2000; 2000US-0638258

HAMILTON C M PRICE J. L. HARGISS T. R. GORLACH J. GORL/) HARG/)

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LEDFORD B L. WOESSNER J F GARCIA C A. MATHEW A V. (LEDF/) (WOES/) (HAAS/) (GARC/) ( MATH/)

540

Haas WD; Hargiss TR, Yu Y; , Woessner JP, H An Y, Hamilton CM, Price JL, Har Page A, Mathew AV, Ledford BL, Gorlach J, Rameaka JG, Garcia CA;

WPI; 2003-102509/09.

Novel Arabidopsis thaliana nucleic acid useful

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transgenic plant with enhanced disease resistance and enhanced traits of interest, as probes, and in diagnosis and screening purposes
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Claim 1; Page 158; 277pp; English.

The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that modulate the expression or function of the polypeptides, for mapping functional composition of cells, preferably plant cells, in screening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or biosynthetic products of withstanding a particular disease or biosynthetic products in plants and to create genetically modified and are useful for introducing or inhibiting production of transgenic organisms, such as plant cells and plants. Transgenic plants are useful for introducing or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as information or improving disease resistance and stress tolerance in plants, screening biologically active agents, such as information or interest or intere biosynthetic pathways of nutritional, commercial or medici. Sequences ABX60655-ABX61554 represent Arabidopsis thaliana polynucleotides of the invention

Sequence 460 BP; 113 A; 103 C; 134 G; 109 T; 1 other;

ij DB 25; Length 460; 1; Indels 11.8%; Score 448; DB 25 ilarity 99.6%; Pred. No. 5e-134; Conservative 0; Mismatches Query Match Best Local Similarity Matches 459;

GCAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 009

460 GCAAGCTCTGGCATCATCACCTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 401

719 GTGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCT 099

839

ABL93850 standard; cDNA; 453 .BL93850/c ESULT 3

10-JUN-2002

ABL93850

(first entry)

Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis; Arabidopsis thaliana nucleic acid sequence Ref:2027615 SEQ ID NO:615.

26-JAN-2001; 2001US-0770444. genetic modification; gene, 27-JAN-2000; 2000US-178502P Arabidopsis thaliana. HAMILTON C M. WOESSNER J.P RAMEAKA J G. RAINES T M. GORLACH J. MATHEW A V. m HURBAN P. US2002023280-A1. ALLEN K. HOFFMAN SLATER 21-FEB-2002 (ALLE/) (HOFF/) (HURB/) PAGE/) MATH/) LEDF/) GORL/) YUYY/) WOES/) HAAS/) RAIN/) SLAT/ 

Haas WD; rice JL, Raines TM, Yu Y; Ledford BL, Weessner JP, Haas Davis KR, Allen K, Hoffman N; Price JL, Ledford BI An Y, Hamilton CM, P. Page A, Mathew AV, Kricker M, Slater T, Gorlach J, A Rameaka JG, Garcia CA, K Hurban P;

WPI; 2002-267486/31.

New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein

Claim 1, SEQ ID 615; 44pp; English.

comprising a sequence capable of hybridishing under stringent conditions.

To a sequence (SI) selected from any one of the 99s sequences given in the 248194334. (I) have insecticide and fungicide activities, and they can be used as protein expression modulators. (I) can be used in identifying homologous or related genes, in producing compositions that modulate the expression or function of their encoded proteins, mapping functional regions of the proteins, and in studying associated physiological pathways (I) can also be used. (I) for the genetic physiological pathways (I) can also be used. (I) for the genetic of thistanding a particularly plant cells, (2) in screening assays of various plant strains to describe environmental stress; (3) for enhancing or inhibiting production of a biosynthetic product in a plant; (4) as probes in mapping and in diagnosis; in genetic modification and conscreening purposes; to generate additional copies of the nucleic The present invention describes an Arabidopsis thaliana nucleic acid (I) acids, to generate ribozymes or antisense oligonuclectides, and as single-stranded DNA probes or as triple-strand forming oligonuclectides; and (5) for generating genetically modified transgenic organisms. for this patent did no btained in electronic Note: The sequence data for this specification, but was obtained

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Sequence 453 BP; 111 A; 100 C; 132 G; 107 T; 3 other;

41.0%; Score 439; DB 24; Length 453; 99.1%; Pred. No. 4e-131; 0; Mismatches Conservative Similarity Query Match Best Local Simi Matches 450;

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PR 27-JUL-1999 990S-0145224.

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PR 22-JUL-1999 990S-0145218.

PR 22-JUL-1999 990S-0145918.

PR 02-AUG-1999 990S-0145918.

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PR 23-SEP-1999 990S-015303.
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258 GACTAPACCGGCTCCGAAGAGCCGACTTCTAAAGACCGTCACACGAAAGTAGAAGACG 317
                                                                                                                                                                                                                                                                                                                                                                                                         315 GTTAGGTCACAAATCCGACGCCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC 374
                                                                                                                                                                                                                                                                                                                                                                                                                             375 GATTATAGCCGCCACGGGTACGGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              438 GATAÁTTGAAGCAACCGGAACCGGAACTGTACCGGCTÁTTGCTGTATCGGTTAACGGAAC 497
                                                                                                                                                                                                                                                                                                                                                  255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA
                                                                                                                                                                                                                                                              0; Gaps
                                                                                                                                                                                                                                  DB 21; Length 1156;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant, 88, gene, transcription factor, transgenic, agriculture, metabolic chemically-emvironmental/etress/drought microbial disease resistance, herbicide/resistance, seed yield fruit yield; growth rate; leaf senescence;
                                                                                                                                                                                                                                 Query Match
14.7%; Score 157.8; DB 21; Length
Best Local Similarity 75.9%; Pred. No. 4.9e-40;
Matches 195; Conservative 0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis cDNA encoding a transcription factor #85
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ABK65233
ID ABK65233 standard; cDNA; 1728 BP.
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PILGRIM M.
CREELMAN R.
DUBELL A J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           435 CTTAAAAATCCCGACGA 451
99US-0160814
99US-0160815
99US-0160981
99US-0160981
99US-0161404
99US-0161405
99US-0161405
99US-0161359
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99US-0161350
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16-NOV-2000, 2000US-0713994.
16-APR-2001, 2001US-0837944.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      498 TTTAAAATCCCGACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana
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                                                                                                                                                                        28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
                           28-FEB-2002,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK65233;
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(CREE/)
(DUBE/)
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ABK65217 standard; cDNA; 1231 BP

RESULT 6 ABK65217

ABK65217;

Keddie J; Pineda O;

Jiang C,

J, Heard J, J Riechmann JL,

f, Creelman R, Dubell AJ, Ratcliff O, Reuber JL, Ri

Pilgrim M,

Adam L,

(YUGG/) (RATC/) (REUB/) (RIEC/)

REUBER J L. RIECHMANN J PINEDA O.

DAM

(JIAN/ ADAM/

HEARD J

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The invention relates to 1 of 232 isolated or recombinant polynucleoticus encoding an Arabidopsis thaliana transcription factor, their variants, encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% complements fragments, or related polynucleotide with 31% to 95% to a wild-type or reference plant, or the plant compared to a wild-type or reference plant, or the plant or whibits an altered phenotype as compared to a wild-type or reference plant, or the plant or wild-type or reference plant, or the plant or a transgenic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynuclectides, a computer of readable medium having stored sequence information selected from one of 46% fully defined sequences of incomation a plant having a homologue sequences given in the specification. The isolated or recombinant polynuclectide is used for producing a plant having a modified trait, the method comprising selecting a plant to overexpress of the polypeptide or antisense nucleic acid, inserting a modified or introducing the vector into a plant or a call of a plant to overexpress introducing the vector into a plant or a call of a plant to overexpress or production of agriculturally useful proteins or metabolic chemicals, microbial disease resistance, herbicide realstance, seed and fruit yield, growth real, leaf and flower senescence and many other traits listed in the received in the present sequence is one of the 232 polynucleotides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   248
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                                                                                                                   An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                540 GCGAGAGCTAGGTCATAAATCCGACGGTGAGACAATAGAGTGGCTTCTTCAACAAGCTGA
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Pred. No. 1.2e-30;
0; Mismatches 70; Indels 0
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                                                                                                                                                                                                                               Claim 4; Page 373-376; 941pp; English
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Best Local Similarity 71.0%;
Matches 171; Conservative
WPI; 2002-292022/33.
P-PSDB; AAU93047.
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encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comparising the polynucleotides, a computer readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to 1 of 232 isolated or recombinant polynucleotides
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keddie J;
Pineda O;
                                                                                                                                       Plant, ss, gene, transcription factor, transgenic, agriculture, metabolic chemical; environmental stress; drought, microbial disease resistance, herbicide resistance; seed yield;
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                                                                                         Arabidopsis cDNA encoding a transcription factor #69.

    Heard J, J
    Riechmann JL,

                                                                                                                                                                                                            fruit yield, growth rate, leaf senescence;
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Ratcliff O, Reuber JL, I
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                                           (first entry)
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P-PSDB; AAU93031.
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DUBELL A J.
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Adam L,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGGATCCGTATGCCTGCTGCTGCTGTCTTTCAGCTCACACGTGAGCTTGGT 358
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATA 381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCGCTACAGGGACTGGAACCATTCCGGCTAACTTCACTTTTAAACATCTCACTTCGT 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAACCTTAAAA 441
plant, and selecting for a modified trait (e.g. increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth rate, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                        262 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGT
                                                                                                                                                                                                                                                                                                                                       0; Gaps
                                                                                                                                                                                                                                                                             Query Match
11.6%; Score 124.6; DB 24; Length 1231;
Best Local Similarity 65.0%; Pred. No. 2.7e-29;
Matches 184; Conservative 0; Mismatches 99; Indels 0;
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25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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16-APR-1999;
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RR 24-JUL-1999; 99US-014521B.

RR 27-JUL-1999; 99US-014521B.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cyclin-dependent protein kinase; CDK; CDC2a; CDC2b; VbDBP; cell cycle; DNA binding protein; interacting protein; environmental stress; growth regulator; herbicide; nematode resistance; plant breeding; ss.
                                                                                                                                                                                                                                                                                                             358 CGGATCCGTATGCCTGCCATGTGTGTGTGTGTTTTTCAGCTCACCTGAGCTTGGT
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Best Local Similarity 65.0%; Pred. No. 2.8e-29;
Matches 184; Conservative 0; Mismatches 99; Indels 0;
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              99US-0160768.
99US-0160814.
99US-0160815.
99US-0160880.
99US-0160980.
99US-0161908.
99US-0161404.
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           (1-OCT-1999)
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Arabidopsis thaliana expressed sequence related polynucleotide #332. Transgenic plant; plant; genetically modified cell; environmental stress; ribozyme creation; disease resistance; 25-FEB-2003 CDC2a 412 ( 331 ABX62217; ESULT 9 BX62217

correction and CDC2b are the only CDK genes to have been characterized in detail in Arabidopsis thaliana. They were used as bait in a two-hybrid screening assay with a cDNA library of a plant cell suspension as prey. The plant cell cycle interacting proteins identified were designated caids, vectors comprising them, the proteins they express, antibodies that bind to them and or inhibitors of their protein expression and/or contriby may be used for modulating the cell cycle in an animal or plant, cycle proteins and/or growth, for influencing the activity of cell cycle proteins in a plant or animal cell, as positive or negative regulators of cell proliferation, for modifying the growth inhibition caused by environmental stress conditions, especially change in a mormal or suboptimal nutrient conditions, especially confined in a conditions, especially confined in a condition of conditions or activators of the conditions of conditions and conditions and conditions and conditions and conditions are activators of conditions and conditions and conditions and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators and conditions are activators. The VbDBP clone is very similar to the A. thaliana putative DNA binding protein and also contains a lot of homologies with Oryza sativa PCF2. VbDBP interacts with cyclin-dependent protein kinase (CDK) CDC2b but not regulatory sequences may be used a markers in plant or animal cell and tissue cultures or as a marker in marker-assisted plant breeding. The regulatory sequences may also be used for the expression of heterologous DNA sequences during a stage of the cell cycle. Nucleic acids encoding plant cell cycle interacting proteins, useful for regulating plant growth and in recombinant DNA protocols plants. The DNA sequences and their herbicides and/or Inze D; Sequence 1081 BP; 302 A; 195 C; 266 G; 318 T; 0 other; Torres Acosta JA, of cell cycle protein, as growth regulators, inducing nematode resistance in plants. The I Claim 1; Page 131-132; 152pp; English. De Veylder L, Boudolf VKCK, CROPDESIGN NV WPI; 2000-431601/37. P-PSDB; AAY96818

232 AAGAGAAGCTCTAACAAAGACAGACACACTAAAGTCGAAGGTAGAGGTCGACGAATTCGG 291 GACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCACG 390 292 ATGCCTGCTCTTTGTGCTGCTAGGATTTTTCAATTGACTAGAGAATTGGGTCATAAATCT 351 352 GATGGTGAAACTATCCAGTGGCTGCTTCAACAAGCTGAGCCATCGATTATTGCAGCTACT 411 271 ATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAATCC Gaps ö Query Match 11.0%; Score 118; DB 21; Length 1081; Best Local Similarity 73.3%; Pred. No. 3.4e-27; Matches 151; Conservative 0; Mismatches 55; Indels 0; 391 GGTACGGGAACGGTTCCCGCCATCGC 416 GGÍTCAGGÁACTATACCGGCCTCTGC 437

ABX62217 standard; DNA; 422 (first entry)

stress tolerance, fungicide screening; insecticide screening gene; da.

Gossypium hirsutum

JS2002040490-A1

04-APR-2002

26-JAN-2001; 2001US-0770423.

7-JAN-2000; 2000US-178512P

HAMILTON C M. GORLACH J. HAMI/

AMEAKA J G RAINES T M. YYYY RAME/

LEDFORD PAGE/) LEDF/ 

KRICKER M HAAS/)

HURBAN P. DAVIS K 1 ALLEN K. HOFFMAN ALLE/) HOFF/) HURB/)

BL, Woesener JP, Haas WD; R, Allen K, Hoffman N; Yu Y; Raines IM, Price JL, Ra Ledford BL, , Davis KR, Gorlach J, An Y, Hamilton CM, 1 Rameaka JG, Page A, Mathew AV, Garcia CA, Kricker M, Slater T,

Hurban P;

Novel Arabidopsis thaliana nucleic acid useful for identifying homologous or related genes, and to create genetically modified and transgenic organisms, such as plant cells and plants WPI; 2003-110411/10.

Claim 1; SEQ ID NO 332; 43pp; English:

The invention describes an Arabidopsis thaliana nucleic acid (I). The polypeptide (II) encoded by (I), transganic plant (III) or genetically modified cell (IV) are useful for screening accandidate agent for its biological effect, by combining the candidate agent with (II), (III) or (IV), and determining the effect of the candidate agent on (II), (III) or producing compositions that modulate the expression or function of its encoded protein, for mapping functional regions of the protein, for studying associated physiological pathways, for genetic manipulation of cells, preferably plant cells, infectening assays of various plant strains to determine the strains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibiting production of biosynthetic product far a plant, for producing polypeptides, as probes for the detection of amancing or inhibiting production of biosynthetic product in a plant, for samples, to generate additional copies of (I), to generate ribozymes or oligonucleotides, as single stranded DNN probes or as tribigle stranding oligonucleotides, and to creat genetically modified and set of the strander of services and the strander of services and strains of coreat genetically modified and set of the strander of services or creat genetically modified and set of the strander of services and strains and the oreat genetically modified and set of the strander of services and services and services or creat genetically modified and set of the services or coreat genetically services and services or creat genetically services and services and services or creat genetically services and services or creat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or coreat genetically services or cor seful for introducing or lawrovens carrive agents, e.g., olerance in plants, screening biological active agents, e.g., occurring Arabidopsis thaliana expressed seguences. Note: The seguence data for this patent did not form part of the printed ransgenic organisms, such as plant cells and plants. (II) or (III) is seeful for introducing or improving disease resistance and stress suhanced tolerance to environmental stress, or to produce a factor. sequence represents a nucleic acid that may correspond to naturally raits of interest, for screening programs, as crops which exhibit oides, insecticides, etc., and for elucidating blochemical is useful as crops for their enhanced diseased resistance.

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               but was obtained in electronic format directly from the
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                                                                                                                                                           Gaps
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Pineda O;
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                                                                                                                       DB 25; Length 422;
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                                                                                                                     Score 111.2; DB 25; Length
Pred. No. 3.3e-25;
0; Mismatches 58; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis cDNA encoding a transcription factor #67
                                                                                     Sequence 422 BP; 111 A; 100 C; 118 G; 93 T; 0 other;
                                                 seggata.uspto.gov/seguence.html?DocID=999909770423.
                                                                                                                                                                                                                                                                                                                                                                                                                                                CTGGAACTGGCACTACTCCGGCGA 270
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                                                                                                                     Query Match
Best Local Similarity 71.6%;
Matches 146; Conservative
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P-PSDB; AAU93029.
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PINEDA O.
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specification,
US patent cff:
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16-APR-2001;
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controlled as compared to a wild-type or reference plant, or the plant exhibits ectopic expression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included care a transgenic plant crampts as compared to a wild plant. Also included readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant equences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a plant having a modified trait, the method comprising selecting a polynucleotide that encodes a polypeptide or an antisense nucleic acid, inserting the polympeptide or antisense nucleic acid, thereby producing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified producing the vector into a plant or a cell of a plant to overexpress the polypeptide or antisense nucleic acid, thereby producing a modified production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistance, herbicide resistance, seed and fruit yield, growth search, leaf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides
                                                                                                                                     The invention relates to 1 of 232 isolated or recombinant polynucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polynucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 268
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                     An isolated or recombinant polynucleotide used to produce a transgenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 269 GGATGCCTGCCACGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    163 GTATGCCAATCATTTGCGCAGCTCGAGTTTTTCAATTGACCAGAGAGTTAGGTCACAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 10.4%; Score 111.2; DB 24; Length 1009; Best Local Similarity 71.6%; Pred. No. 5.2e-25; Matches 146; Conservative 0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hybridisation assay, genetic mapping, gene expression control, protein identification, signal transduction pathway, metabolic pathway, promoter, termination sequence, ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1009 BP; 256 A; 212 C; 267 G; 274 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana DNA fragment SEQ ID NO: 4718.
                                                                                           Claim 4; Page 309-310; 941pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 CGGGTACGGGAACGGTTCCCGCCA 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 credahcredchcracriccedceh 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAC33900 standard; DNA; 1486 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                               plant
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rraagaaaccaccercraaagarceacacacaaagrreaceeaagaagaagaagarre 209
                                                                                                                                                                        269 GGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAAT 328
                                                                                                                                                                                                                                                           CCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCA 388
                                                                                                                                                                                                        GIATGCCAATCATTTGCGCAGCTCGAGTTTTTCAATTGACCAGAGAGTTAGGTCAAGT
                                                                                     ccarrograndancanagacidecrirciccercaacidaaccironarcanagaccea
    DB 21; Length 1486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought;
               .4e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis cDNA encoding a transcription factor #205
  Score 111.2;
Pred. No. 6.46
0; Mismatches
                                                                                                                                                                                                                                                                                                                                              CGGGTACGGGAACGGTTCCCGGCCA 412
                                                                                                                                                                                                                                                                                                                                                                                       CTGGAACTGGCACTACTCCGGCGA 353
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ID ABK65353 standard; cDNA; 1172
  10.4%;
ilarity 71.6%;
Conservative
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Query Match
Best Local Similarity
Matches 146; Conserv
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The invention relates to 1 of 232 isolated or recombinant polynucleotides of encoding an Arabidopsis thallana transcription factor, their variants, or encoding an Arabidopsis thallana transcription factor, their variants, or encoding an Arabidopsis thallana transcription factor, their of 95% sequence identity, where the plant possesses an altered trait as compared to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant comprise a scongared to a wild plant exhibits an altered compression or altered expression of one or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polynucleotides, and identifying a homologue sequence from a database comprising a polynucleotide from one of sequences comprising inputting sequence. Information selected from one of sequences comprising inputting sequence information selected from one of the fully defined sequences given in the specification. The isolated or recombinant polynucleotide is used for producing a polynucleotide that encodes a polypeptide or antisense nucleic acid into an expression vector.

Combinate polypeptide or antisense nucleic acid into an expression vector. Introducing the vector into a plant or a cell of a gariculturally useful proteins of acid increased plant, and selecting for a manisense nucleic acid into an expression vector. Computation of agriculturally useful proteins of a compute of agriculturally useful proteins of a draw of agriculturally useful proteins of a draw of a gariculturally useful proteins of a compute of agriculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful proteins of a draw of a gariculturally useful p
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Pred. No. 2.38-21;
0; Mismatches 65; Indels 0;
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Riechmann JL, Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1172 BP; 331 A; 217 C; 251 G; 373 T; 0 other;
microbial disease resistance; herbicide resistance;
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Ratcliff O, Reuber JL, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MENDEL BIOTECHNOLOGY INC.
                                      fruit yield; growth rate; leaf
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Best Local Similarity 68.1%;
Matches 139; Conservative
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16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
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                                                                                                                  Arabidopsis thaliana
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P-PSDB; AAU93167.
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Adam L, Ra
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(REUB/
(RIEC/)
(YUGG/)
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KEDD/
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us-09-938-842a-1034.rng

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The invention relates to 1 of 232 isolated or recombinant polymucleotides encoding an Arabidopsis thaliana transcription factor, their variants, complements, fragments, or related polymucleotide with 31% to 95% sequence identity, where the plant possesses an altered trait as compared
                                                                                       328
312 CAGATGGCCAAACAATTGAATGGTTACTTCGTCAAGCAGAGCCTTCTATTATAGCTGCAA 371
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An isolated or recombinant polynucleotide used to produce a transgenic
plant -
                                                                                                                                 252 GTATGCCGATTATATGTGCTGCTCGTGTTTTTCAGCTAACGAGAGGCTTGGTCATAAGT
                                          192 TGAAGAAACCACCGGCGAAAGATCGACATAGCAAAGTCGATGGAAGAGGGAGAAAGATCC
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Pineda O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant; ss; gene; transcription factor; transgenic; agriculture; metabolic chemical; environmental stress; drought; microbial disease resistance; herbicide resistance; seed yield; fruit yield; growth rate; leaf senescence; flower senescence.
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Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis cDNA encoding a transcription factor #68.

    Creelman R, Dubell AJ, Heard J, J
Ratcliff O, Reuber JL, Riechmann JL,

                                                                                     GGATGCCTGCCACGTGTGCGGCTAGGATTT
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                                                                                                                                                                                                                                                                   CGGGTACGGGAACGGTTCCCGCCA 412
                                                                                                                                                                                                                                                                                                           caddaacrddracaacrddadda 395
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16-NOV-2000; 2000US-0713994.
16-APR-2001; 2001US-0837944.
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RIECHMANN J 1
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PINEDA O.
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P-PSDB; AAU930303
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Adam L, Ra
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209
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CREE/)
DUBE/)
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to a wild-type or reference plant, or the plant exhibits an altered phenotype as compared to a wild-type or reference plant, or the plant exhibits eccopic expression or altered expression or more genes associated with a plant trait as compared to a wild plant. Also included are a transgenic plant comprising the polymucleotides, a computer or readable medium having stored sequence information, and identifying a homologue sequence from a database comprising a plurality of known plant sequences comprising inputting sequence information selected from one of 464 fully defined sequences given in the specification. The isolated or recombinant polymucleotide is used for producing a plant having a modified trait, the method comprising selecting a polymucleotide that encodes a polypeptide or an antienne nucleic acid, inserting the coopyration of an antienne nucleic acid into an expression vector, introducing the vector into a plant or a call of a plant to overexpress the polypeptide or antienne nucleic acid, thereby producing a modified production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. increased producing a plant plant or a call of a increased production of agriculturally useful proteins or metabolic chemicals, pest tolerance, environmental stress response (e.g. drought), microbial disease resistence, herbicide resistance, seed and fruit yield, growth rate, lasf and flower senescence and many other traits listed in the specification). The present sequence is one of the 232 polynucleotides encoding an A. thaliana transcription factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ô
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        248 AAGGAAGAGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            361 cacereaerracaacacaaarceeaceeeeaeacraracaareeereereereeracaacaacee 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCATCATCAACGGCGTCAGAACGTCGAAACTTCAAGACCTTTCCAAGTAAATCCCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               128 TGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTCTTTCAATGTCTTTAGCTCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGTCACACGAAGGTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
9.2%; Score 98.6; DB 24; Length 1263;
Best Local Similarity 55.4%; Pred. No. 6.9e-21;
Matches 191; Conservative 0; Mismatches 154; Indels 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1263 BP; 339 A; 305 C; 280 G; 339 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana DNA fragment SEQ ID NO: 41952.
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PR 12-UL-1999; 9908-0142977.

PR 12-UL-1999; 9908-0142977.

PR 13-UL-1999; 9908-01440085.

PR 16-UL-1999; 9908-01440085.

PR 16-UL-1999; 9908-01440085.

PR 19-UL-1999; 9908-01440085.

PR 19-UL-1999; 9908-01440085.

PR 19-UL-1999; 9908-0144331.

PR 19-UL-1999; 9908-0144331.

PR 19-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 20-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-0144331.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014731.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014591.

PR 22-UL-1999; 9908-014932.

PR 22-UL-1999; 9908-014932.

PR 22-UL-1999; 9908-014932.

PR 23-AUG-1999; 9908-014932.

PR 23-AUG-1999; 9908-014932.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

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PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-014992.

PR 23-AUG-1999; 9908-01998.

PR 23-AUG-1999; 9908-01998.

PR 23-AUG-1999;

16-NOV-2001; 2001WO-US43101 16-NOV-2000; 2000US-249222P.

WO200240688-A2 23-MAY-2002 Walker EL, Dellaporta WPI; 2002-490144/52. P-PSDB; ABB83920.

(UYYA ) UNIV YALE

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CAGATGGCCAAACAATTGAATGGTTACTTCGTCAAGCAGAGCCTTCTATTATAGCTGCAA 374
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCA
                                                                                                                                                                                                                                                                                                                                                                                                               DB 21; Length 1379;
                                                                                                                                                                                                                                                                                                                                                                                                                                      58;
                                                                                                                                                                                                                                                                                                                                                                                                                            4e-19;
                                                                                                                                                                                                                                                                                                                                                                                                             8.7%; Score 93.2; D
68.8%; Pred. No. 4e-1
ive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGATGCCTGCCACGTGTGCGGCTAGGATTT
900S-0158029
                        9US-0158369
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                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Matches 128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255
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                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 15
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The invention relates to an isolated nucleic acid molecule (1), maize yellow stripe 1 (ys1) or yellow stripe1-like (ys1) from Arabidopsis (ABN85763-ABN85771). (1) is useful for generating transgenic plants which metal or heavy metal contaminate from soil and for bioremediation of metal or heavy metal contaminated soil. (1) may also be used to aler the distribution of iron within the plant body so that edible parts of crop plants brave more iron. Transgenic plants may also be used in conventional plant breeding schemes to produce progeny which also contain the gene of interest. The present sequence is that of the Arabidopsis ysl encoding cDNA of the invention.

Sequence 83698 BP; 26295 A; 15150 C; 15104 G; 27149 T; 0 other;

Gaps

ö

Score 89; DB 24; Length 83698; Pred. No. 8.3e-17; 0; Mismatches 70; Indels 0

New yellow stripel and yellow stripel-like genes, useful for altering the distribution of iron within the plant body so that edible parts of crop plants have more iron, or for producing plants useful in enhancing iron uptake from soil

Claim 1; Page 114-159; 187pp; English

18741 GTTACCTCCACTCTGTGCAGCAAGGATTTATCAATTGACTAAAGAATTAGGTCACAAATC 18800 18801 adanddrdagacnchigaanddhigchrchacandchgadddanddanchcnchdchd 18860 210 GAAGAGGCTTCGACTAAAGACCGTCACACGAAGGTTGAAGGAAAGAGGAGAAGGATACG 330 CGACGGCGAAACGATTCGGTGGTTGTTGGAGAAACGCTGAGCCGGCGATTATAGCCGCCAC 270 GATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAATC Search completed: February 1, 2004, 21:58:51 Job time : 322.739 secs 18861 TGTAATGGTATCAAACCCAC 18881 390 GGGTACGGGAACGGTTCCCGC 410 Query Match
Best Local Similarity 65.2%;
Matches 131; Conservative 셤 셤 ઠે 셤 ઠ ઠે 8 388 268 254 328 CAATTAACTCGAGAGTTAGGTCACAAAT Gaps ö

Maize; transgenic; plant; yellow stripel-like; yel; Arabidopsis; iron uptake; bioremediation; yellow stripe 1; yel; gene; ss.

Arabidopsis sp

Arabidopsis yellow stripel-like 4 encoding cDNA SEQ ID NO 9.

(first entry)

21-OCT-2002

ABN85767;

ABN85767 standard; cDNA; 83698 BP.

us-09-938-842a-1034.rni

Page 1

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; IMMEDIATE SOURCE:
; CLONE: pTZgpt-F18
US-08-232-463-14
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Sequence 14, Appl
                                                                                                                                                                                                                                        February 1, 2004, 21:45:16; Search time 70.5426 Seconds (without alignments) 6701,220 Million cell updates/sec
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Sequence 57, Appl
Sequence 57, Appl
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Sequence 12199,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 atggcgacaattcagaagct.........cacggtcatcgaaccactga 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 546
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Sequence 6,
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Sequence 57
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1: \cgn2 & \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose \choose 
GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-620-312D-546
US-07-982-712-195
US-09-125-619-3
US-08-125-619-3
US-08-125-528D-1
US-08-998-416-436
US-09-211-0178-74
US-09-211-0178-74
US-09-21-0178-74
US-09-21-0178-74
US-09-26-315-57
US-09-265-315-57
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       569978 segs, 220691566 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                  OM nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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Score Match Length DB ID
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Maximum DB seq length: 200000000
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9 1288
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Perfect score:
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Sequence 5, Appli Sequence 348, App Sequence 2, Appli Sequence 79, Appli Sequence 79, Appli Sequence 3, Appli Sequence 3, Appli Sequence 6, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 17, Appli Sequence 17, Appli Sequence 17, Appli Sequence 27, Appli Sequence 2, Appli Sequence 2, Appli		
55 10 10 10 10 10 10 10 10 10 10	VIRUS	00 reion#1:25
4 US-09-294-5318-5 1 US-09-620-312D-348 1 US-08-8759-444-2 3 US-08-60-89-1 3 US-09-63-7028-79 3 US-09-103-840A-1 2 US-09-103-840A-1 3 US-09-103-840A-1 3 US-09-122-632-8 4 US-09-122-632-8 5 US-09-122-632-8 6 US-09-122-632-8 7 US-09-13-2948-1105 8 US-09-13-13-2948-17 8 US-09-453-7028-11 4 US-09-453-7028-11 8 US-09-453-7028-11 8 US-09-453-7028-17 8 US-09-453-7028-17 8 US-09-453-7028-17 8 US-09-453-7028-17 8 US-09-453-7028-17 8 US-09-453-7028-17 8 US-09-453-7028-17 8 US-09-443-7058-17 8 US-09-443-7058-17 8 US-09-443-7058-17	ALIGNMENTS 232463 INANT FOWLPOX VI	Suite 5 Dos 170, Ve 2,463 5,313 4,300.6
4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	ion US// , F LINGER, E, F G R, F G S: RECOI S: 52 RESS:	ADDRESSEE: Foley & Lardner STREET: 1800 Diagonal Road, CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria CITY: Alexandria COMPUTER: BADABLE FORM: MEDIUM TRE: FLOSYMS-ENGYTARE: PATENTIN DATE: PATENTINO DATE: APPLICATION NUMBER: US/07/93 FILING DATE: 26-AGG-1991 APPLICATION NUMBER: US/07/93 APPLICATION NUMBER: US/07/93 APPLICATION NUMBER: US/07/93 APPLICATION NUMBER: US/07/93 APPLICATION NUMBER: 26-AGG-1991 APPLICATION NUMBER: 26-AGG-1991 APPLICATION NUMBER: 39-768 REGISTRATION NUMBER: 39-768 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INF
aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	1 1 463-14  uence 14, Application Uence 14, Application UEAL INFORMATION: APPLICANT: BORNER, F. APPLICANT: FAPLICANT: PARELINOR APPLICANT: FALKNER, F. TITLE OF INVENTION: REVIGENCE. TOTALE OF SEQUENCES: 5 CORRESPONDENCE ADDRESS: 5	ADDRESSEE: Foley & L STREET: 1800 Diagona CITY: Alexandria CITY: Alexandria CITY: Alexandria COUNTRY: USA COUNTRY: USA COMPUTER READABLE FORM: MEDIUM TYPE: PLOPPY COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC COMPUTER: IBM PC CATOR NUMBER: PRILING DATE: APPLICATION NUMBER: PRILING DATE: APPLICATION NUMBER: PRILING DATE: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: APPLICATION NUMBER: REGISTRATION NUMBER: REGISTRATION NUMBER: REPERENCE/DOCKET NUMBER: REGISTRATION NUMBER: REPERENCE/DOCKET NUMBER: REPERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATIELEPROME: (703) 836-4178-418-418-418-418-418-418-418-418-418-41
60014797678800144444	SULT 1 -08-232-463-14 Sequence 14, Applicat Sequence 10, Sp1060 GENERAL INFORMATION: APPLICANT: DORNER APPLICANT: SCHEIF APPLICANT: SCHEIF APPLICANT: SCHEIF APPLICANT: TURBE APPLICANT: TURBE APPLICANT: TURBE APPLICANT: TONENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD	ADDRESSEE: STREET: 180 CITY: Alexa CITY: Alexa STATE: VA COUNTRY: UG. ZIP: Z2213- COMPUTER READA MEDIUM TYPE: COMPUTER: IF COMPUTER: IF COMPUTER: PREDIUM TYPE: COMPUTER: PREDIUM TYPE: COMPUTER: PREDIUM TYPE: CLASSIFICATION: PRILING DATE: APPLICATION: FILING DATE: APPLICATION: FILING DATE: APPLICATION: FILING DATE: ATTORNEY/AGENT: NAME: BENT, REFERENCE/DON TELEPHORE: TELEP
	RESULT US-08- Sequ Pate Pate AA AA	. אם או או או או או או או או או או או או או

4.1%; Score 44; DB 1; Length 7218;

Query Match

TELEFAX: (703)683-4109
TELEY: 899149
INPORMATION FOR SEQ. IN NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single

linear

TOPOLOGY:

IMMEDIATE SOURCE:

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542 CCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGATCCAACCTCCGC 601
                                                                                                                                         661
                                                                                                                                                                                                         662 GGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAAA
                                                                                                                                                                                                                                                                                                                                                           782 CGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAAG
                                                                                                                               602 AAGCICIGGCAICATCCACIGIGGCICAGCAACTICIGCCGCAAGGAAIGIATCCGAIGI
                                                                                                                                                                                                                                                                                                             TCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGGCGGCCGCTGCTTCGCCGT
                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                             INGTICCAAGCAGCGCTITGTAICCGTITCAGACGTIAGCGGTICGAAITIAI 895
                           .
Best Local Similarity 2.3%; Pred. No. 0.0011;
Matches 8; Conservative 203; Mismatches 143; Indels
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRAIT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: STAINNER, F. G.
APPLICANT: FLIXNER, F. G.
NUMBER OF INVENTION: RECOMBINANT FOWLPOX VIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30472/114 IMMU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1800 Diagonal Road, Suite 500 CITY: Alexandria STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 INP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
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EDNESS: single
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STRANDEDNESS:
TOPOLOGY: li
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APPLICANT: MATC. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 10.7196.136
CURRENT PILING DATE: 10.999-0.2-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-0.2-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-0.2-18
PRIOR PILING DATE: 1998-0.2-18
PRIOR PILING DATE: 1998-0.2-18
PRIOR PILING DATE: 1998-0.2-18
PRIOR PILING DATE: 1998-0.2-18
PRIOR PILING DATE: 1998-0.2-18
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                                                                                                                                                                         255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA 314
                                                                                                                                                                                                                                                                                                                                                                                               GATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATGTCGGTTAACGGAAC 434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 435 CTTAAAAATCCCGACGACGACGAACGCTGATTCTGATATGGGTGAAAATCTGATGAAGAA 494
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         70 ccaadcrosaacactrosacctraraccaccaccacceacceacceacceaccaccrosaccacc 129
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                                                                                                                                                                                                                                                                                                                315 GTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   495 GAAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGACGCCGTTTCAGCTTC
                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; LOCATION: (291); OTHER INFORMATION: Identity of nucleotide at the above locations are US-09-252-991A-8192
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0
                                                                    Length 7218;
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49.2%; Pred. No. 2.1;
tive 0; Mismatches 90; Indels
                                                                                                            Indela
                                                             Query Match
3.8%; Score 41; DB 1; Le
Best Local Similarity 2.2%; Pred. No. 0.01;
Matches 8; Conservative 205; Mismatches 150;
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US-09-252-991A-8192
; Sequence 8192, Application US/09252991A
; Patent No. 6551795
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ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
, CLUNE: PTZGPt-Fls
US-08-232-463-14
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Best Local Similarity
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3941480 CTGGCGGACAAGGCGCCCCCGGGGGTGCTGGCGGGCCCGGCGCCGATAACCCCACCGGCA 3941539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1076 GNTGYTGYGTNGARGCNGCNGCNGARWSNGGNGGNTGYGTNATGGCNGCNGCNACNGGNC 1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .256 TNTGYGGNAAYGGNTTYGTNGARGCNGGNGARGARTGYGAGYTGYGGNCCNGGNCARGART 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          637 CTGCCGCAAGGAATGTATCCGATGTGGGCTATTCCATCAAACGCAATGATTCCGACGGTC 696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      817 ATGGCTAGACCACCTCCTTTACAAGTTGTTCCAAGCAGCGGCTTTGTATCCGTTTCAGAC 876
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                                                                                                                                                                                      133 CTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTCAATGTCTTTAGCTCCACCGTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               697 GGAGCTITCTTCTTGATTCCACAAATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCT
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                                                                                                                                     Gapa
                                                                                 DB 3; Length 4403765;
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                                                                                                                                   37; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.0%; Score 32.2; DB 4; Length 225.2%; Pred. No. 4.1;
tive 47; Mismatches 197; Indels
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                                                                                                                                                                                                                                                                                                                                          3941540 rcaccacacaccacacacacacacacacacacacacas 3941571
                                                                                                                                                                                                                                                                                           193 TCGACAGGACCACCATTGAAGAGAGCTTCGAC 224
                                                                               Score 32.8; DE
Pred. No. 68;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: 99-39
CURRENT APPLICATION NUMBER: US/09/632,098
CURRENT FILING DATE: 2000-08-02
NUMBER OS SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 3.0
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     ) OTHER INFORMATION: represent a, t, c US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: (1)...(2400)
OTHER INFORMATION: n = A,T,C or G
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 6, Application US/09632098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Artificial Sequence
                                                                               Query Match 3.1%;
Best Local Similarity 59.8%;
Matches 55; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Sheppard, Paul O. APPLICANT: Balindur, Nand APPLICANT: Bishop, Paul D. TITLE OF INVENTION: MAMMALIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3.0%
Best Local Similarity 25.2%
Matches 82; Conservative
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LOCATION: (1)...(2406)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 5
LENGTH: 2406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-632-098-5
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                                                                                                                                                                                                                                                                              PPLICANT: Marc J. Rubenfield et al.
ITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
ITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: (2266)
COTHER INFORMATION: Identity of nuclectide at the above locations are unknown.
JS-09-252-991A-8112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2487 CCAAGCTGGAACAGCTGGAGGCCTATAGCAGACGACGCCCACCGGGAGGGCCCTGAGGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   111 CCAAGTAAATCCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTC 170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     171 AATGTCTTTAGCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGGTTCGACTAAAGA 230
130 AATACCGGCACCCGCATCGCCGATAACCAGAACACCCTGAAGGCCGGCGAGCGCGGGACCG 189
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OTHER INFORMATION: "n" bases at various positions throughout the sequence
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                                                                                                    190 redrigeredakoacricareardededakoareaceaerredaededede 246
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APPLICANT: FRASER, John C.
IIILE OF INVENTION: DNA SOUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILLE OF INVENTION: TUBERCULOSIS
FILE OF INVENTION: TUBERCULOSIS
                                                   Score 33; DB 4; Length 2874;
Pred. No. 2.5;
0; Mismatches 90; Indels
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR PILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR PILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 8112
LENGTH: 2874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
                                                                                                                                                                                                                          quence 8112, Application US/09252991A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ch 3.1%;
1 Similarity 49.2%;
87; Conservative (
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SOFTWARE: Patentin Ver. 2.1
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Best Local Similarity
Matches 87; Conserva
                                                                                                                                                                                                         2-991A-8112/c
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TYPE: DNA
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3947108 GCGGACAAGGCGGCGCCGGGGGGTGCTGGCGGGCCCGGCGCCGATAACCCCCACCGGCATCG 3947167
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                                    Gaps
                                                                                                                                                                                                                                                                     ALFALICANT: Choi et. al.
TITLE OF INTENTION: Streptococcus pneumoniae Antigens and Vaccines
WUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSER: Human General
DB 3; Length 4411529;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.9%; Score 30.6; DB 3; Length 412; 53.8%; Pred. No. 5.5;
                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HP vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
                                  36;
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 Score 31.4; D
Pred. No. 95;
0; Mismatches
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                                                                                                                                            196 ACAGGACCACCATTGAAGAGAGCTTCGAC 224
                                                                                                                                                                                                                                                                                                                                                        STREET: 9410 West Avenue STATE: Rockville STATE: Maryland COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,083
                                                                                                                                                                                                                                                                    Sequence 111, Application US/08961083
Patent No. 6159469
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2.9%;
ilarity 59.6%;
Conservative
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ATTORNEY/AGENT INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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REGISTRATION NUMBER: 3
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nucleic acid
EDNESS: double
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Matches 63, Conservative
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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                 Similarity
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APPLICANT: Choi e
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 Query Match
Best Local Simil
Matches 53; C
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US-08-961-083-111
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Patent No. 65730
                                                                                                                                                                                                                                   RESULT 9
US-08-961-083-111
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Sequence 195, Application US/08961527
Patent No. 6420135
Ormanac, Radoje T
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APPLICANT: Charles Kunsch
TITLE OF INVENTION: Strep
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ATTORNEY/AGENT INFORMATION
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FORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Diskette,
COMPUTER: HP Vectra 48:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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REGISTRATION NUMBER:
                                                           LE REFERENCE: 784CIP2B
                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                          ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..
US-09-620-312D-546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Choi et. al.
TILE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
NUMBER OF SEQUENCES: 452
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 858 CITIGIAICCGITICAGACGIIAGCGGIICGAAITIAICAAGAGCGACGICGGIIAI 914
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
COMPUTER: HV vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
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53.8%; Pred. No. 5.5;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/536,784
FILING DATE: 30-Oct-1997
FLASSIFICATION: CURNOWN:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/961,083
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE DESCRIPTION: SEQ ID NO: 111: JS-09-536-784-111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: OCT-30-1997
ATTORNEY/AGENT INFORMATION:
NAME: MICHAELLE S. MATKE
REGISTRATION NUMBER: 41,971
REFERENCE/DOCKET NUMBER: PB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -312D-546/c
e 546, Application US/09620312D
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: 111
SEQUENCE CHARACTERISTICS:
LENGTH: 412 base pai:
                                                                                                                                                                                                                                                                                                              SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
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Best Local Similarity 53.8
Matches 63; Conservative
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NUMBER OF SEQUENCES: 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7 ACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTTGATCTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 ACCATCATCAACGCGTCAGAACGTCGAAACTTCAAGACCTTTCCAAG 115
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No. 6569662el Nucleic Acids and Polypeptides
                                                        CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-04-25
PRIOR PILING DATE: 2000-01-21
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: Dt_ FL_Genes Version 1.0
SOFTWARE: Dt_ FL_Genes Version 1.0
LENGTH: 1288
                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
2.9%; Score 30.6; D
Best Local Similarity 55.0%; Pred. No. 9.9;
Matches 60; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JAI COUNTRY; USA
STREET: 9410 Key West Avenue
STRIE: Maryland
COUNTRY; USA
STRIE: Maryland
ZIP: 200"
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,527
FILING DATE:
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821 AGAACTTCGACGGCAGCTTCCGCGGCTCCGCCCAGGGCATCGAGGGCAGCATCAGGAGCC 880
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US-08-545-528D-1/G
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                                                                                                                                                                                                                                       2137 chirchchardacdacardhhardachacadachardadadhacarararthah 2081
                                                                                                                                                                                                       858 CTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGAGCGACGTCGGTTAT 914
                                                                                               Gaps
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                                                         DB 4; Length 6693;
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                                                                                                                                                                                                                                                                                                                       Sequence 1. Application US/07982712

Patent No. 5456391

CENERAL INFORMATION:

APPLICANT: Hideys FUJIMOTO, Kimiko ITOH

APPLICANT: Mikihiro YAMAMOTO, and Ko SHIMAMOTO

TITLE OF INVENTION: Insecticidal Protein-encoding Gene,

TITLE OF INVENTION: Plants Transformed with the Gene, an NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Wenderoth, Lind & Ponack

STREET: 805 Fifteenth Street, N.W., #700

CITY: Washington

STRIES D.C.
                                                                                             54; Indels
                                                         Score 30.6; DB
Pred. No. 23;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIF: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 144 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2.8%; Score 30.4; Dilarity 54.5%; Pred. No. 15; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear OLECULE TYPE: other nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                       7.9%;
Local Similarity 53.8%;
Les 63; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Wordperfect 5.1
URRENT APPLICATION DATA:
APPLICATION NUMBER: US/07,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2172 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 1 to 2172
IDENTIFICATION METHOD:
OTHER INFORMATION:
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REGISTRATION NUMBER; 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19921127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUCLEIC ACID
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CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME/KEY: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 61; Conserva
; TOPOLOGY: linear
US-08-961-527-195
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                                                       Query Match
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880 AGCGGTTCGAATTTATCAAGAGCGACGTCGGTTATGGCTCC

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GENERAL INFORMATION:
APPLICANT: Fraser et al.
TILLOANT: Fraser et al.
TILLOANT: Fraser et al.
TILLOANT: Fraser et al.
TILLOANT: Fraser et al.
Patent No. 633773
TILLOANT: Thereof, and Uses Thereof
FILLS PATENTION: Thereof, and Uses Thereof
CURRENT APPLICATION NUMBER: US/08/545,528D
CURRENT FILING DATE: 1995-10-19
PRIOR APPLICATION NUMBER: US 08/483,018
PRIOR APPLICATION NUMBER: US 08/473,545
PRIOR PILING DATE: 1995-06-07
NUMBER OF SED ID NOS: 1
SOFTWARE: Patentin version 3.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3151 CCTTATCAGCAGCCTTCGCAGCACCAGCATTATCCACAACTTCTCCAATTGCAGCACCTC
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                                                     881 CGCACCTCATGGACATCCTCAACAGCATCACCATCTACACCGACGCCCACAG
940 ACAACCGGTAGTTCATCGTCAATTGCAACAACAACGACGCACACGCTGAGAG 991
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                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: BARBOUR, ALAN G.
APPLICANT: WEINSTOCK, GEORGE M.
TILLE OF INVENTION: WP-LIKE SEQUENCES OF PATHOGENIC BORRELIA
FILE REFERENCE: UTSH: 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/125,619
CURRENT FILING DATE: 1999-01-27
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Patent No. 6537773
                                                                                                                                                                                          pplication US/09125619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: DNA ORGANISM: Borrelia burgdorferi
                                                                                                                                                                                                                                                                                                     JING-REN, ZHANG
HARDHAM, JOHN M.
HOWELL, JERRILYN K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 48.3%;
Matches 85; Conservative
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US-08-545-528D-1
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	0; Gaps
80073;	0
Length 5	Indels
B 4;	106;
Query Match 2.8%; Score 30.4; DB 4; Length 580073; Best Local Similarity 47.0%; Pred. No. 2.1e+02;	0; Mismatches 106;
2.8%;	ative
ilarity	94; Conservative
ch 1 Sim	94;
Query Mai Best Loca	Matches

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Gaps	TCAAGC	TCTTT	CTGAGA
·. 5	CGAGG	CATGO	ACACG
THOSTS	TTATGGCTC	CAATIGITC	CAACGACGC
, oo T	CGTCGG	ACTCAA	CAACAA
circa (1) competyactve of Hismacones 100; Indels of daps 0;	871 TCAGACGTIAGCGGTTCGAATTTATCAAGAGCGACGTCGGTTATGGCTCCGAGCTCAAGC 930	3402 ICACTCTTTCCATTACAGAGAAATCAGGAACAAACTCAACAATTGTTCCATGCTCTTTT 3343	931 TCAGGCGTAACAACCGGTAGTTCATCGTCAATTGCAACAACAACGACGACACGCTGAGA 990
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א מידי א מידי	AGCGGTTC	тссаттас	ACAACCGG
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<sup>3342</sup> TCAGAGTTACCTTCTTGGACCAAATCTCCAATTACCTTTCCTCCATCGCTAAAGCTGAGA 3283 

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<sup>1051</sup> GCACGGTCATCGAACCACTG 1070

<sup>3222</sup> ACTGATGCACCAACACGTG 3203

Search completed: February 2, 2004, 03:00:11 Job time: 101.543 secs

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Sequence 502, Api
Sequence 615, App
Sequence 257, App
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l atggcgacaattcagaagct......cacggtcatcgaaccactga 1071
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Sequence 1
Sequence 1
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Sequence 2
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                                                                                                                                                                                                                                                                                                                                                                 Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/USO7_NEW PUB.seq:*
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13: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
14: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
15: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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16: /cgn2_6/ptodata/2/pubpna/USO9_NEW PUB.seq:*
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US-09-938-842A-1034
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US-10-225-068-165
US-09-934-455-137
US-10-302-267-61
US-10-225-068-245
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US-09-770-696-257
                                                                                                                                                         Potal number of hits satisfying chosen parameters:
                                                                                                               2434939 seqs, 1822278265 residues
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Maximum Match 100%
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Gapop 10.0 , Gapext 1.0
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Match Length DB
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2 10.4 1009 16 US-10-278-536-203	9.8 819 12 US-10-260-238-383 Sequence 383,	00 9.3 1172 11° US. 09-934-455 461° 100 100 8equence 461,	.2 1263 11 US-09-934-455-135 Sequence 135,	13% US-10-225-068-181	7.4 419 10 US-09-878-574-4107 Sequence 4107	7.2 612 12 US-10-260-238-5623 Sequence 5623	6.3 552 12 US-10-260-238-65	4.7 228 12 US+10-260+238-5848 - Sequence-5848	12 US-10-260-238-5405 Sequence 5405	9 US-09-770-444-761	.4 3316 15 US-10-242-056-58 Sequence 5	.2 654 8% US-08-781-986A-613 Sequence 613	.1 629 13 US-10-027-632-221892 Sequence 22	.1 629 14 US-10-027-632-221892 Sequence 22	.1 469 9 US-09-864-761-4365 Sequence 4365,	.2 3.1 828 15 US-10-156-761-5087 Sequence 508	.1 1893 15 US-10-128-714-7597 Sequence 7597	.2 3.1 9025608 15 US-10-1568761+10 Sequence 1,	3.1 671 15 US-10-184-644-346 Sequence 346,	.1 671 15 \US=10-184-634-346 \	3.1 1265 15 US-10-198-846-6773 Seguence 6773	.6 3.0 656 13 US-10-027-632-151527 2 Sequence	.6 3.0 656 14 US+10-027-6324151527 Sequence 1515	.6 3.0 846 12 US-10-320-797-2065 Sequence	.6 3.0 1019 12 US-10-320-797-1065 Sequence	.6 3.0 2320 15 US-10-268-441-5 3.0 2320 15 US-nence	-320-797-65 Sequence	.4 3.0 1200 10 US-09-887-576-731 Sequence	15 US-10-268-441-3 Seguence	
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(without alignments) 9695.297 Million cell updates/sec

February 1, 2004, 21:42:55 ; Search time 402.599 Seconds

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ritle:
Perfect score:

OM nucleic - nucleic search, using sw model

Run on:

GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

## ALIGNMENTS

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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Kreps, Joe1
APPLICANT: Zhu, Tong
ITILE OF INVENTION: SAME, AND METHODS OF USE
FILLE OF INVENTION: SAME, AND METHODS OF USE
FILLE REFRENCE: SCRIP1300-3
CURRENT PILING DATE: 2001-08-24
FRIOR APPLICATION NUMBER: US 60/227, 866
FRIOR APPLICATION NUMBER: US 60/227, 866
FRIOR PILING DATE: 2001-01-16
FRIOR PILING DATE: 2001-01-16
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Sequence 1034, Application US/09938842A
Patent No. US20020160378A1
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Best Local Similarity 100.0%;
Matches 1071; Conservative 0
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121 CCCACAGTGAGTCTCGAGGCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 180 	1 GCTCCACCGTCTTCGACACACACCACTGAAGAGAGCTTCGACTAAAGACCGTCACACG		41 AAGGTTGAAGGAAGAGAGAGAAGGATACGGATGCCTGCCACGTGTGGGGGCTAGGATTTTT 300	301 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAAGGATTCGGTGGTTGTTGGAG 360 	61 AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATG 420		421 TCGGTTAACGGAACCTTAAAAATCCCGACGACGACGACGCTGATTCTGATATGGGTGAA 480 	481 AATCTGATGAAGAAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGAC 540	81 AATCTGATGAAGAAAGGAACGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGGGGAC 540	541 GCGGTTTCAGCTTCCTCGGTTTAGCTCCAACGACGACGACGACGACCAACCTCCG 600	CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 6		51 IGGGCTATICCAICAAACGCAAIGATICCGACGACGGGGGCTTTCTTCTTGATICCACAA 720	661 idadetariccarcaaacacaardariccaacagicagacrircricricariccacaa 720	721 ATGGCTGGTCGGTGGATCAGCCTCAGTTATTAGCTTTTCCGGCGCGCGC	0/ 0/00では、10では、10では、10では、10では、10では、10では、10では、	781 TGGTTAGGTGGCGCGGTTCAACAGGGTTCCACGATGGGTAGACCACCTTTAGAA 840 781 TGGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTAGAA 840 ·	-	841 GTIGTICCAAGCAGCGGCTITGTATCCGTTTCAGCGGTTAGCGGTTCAATTTATCAAGA 900	_	901 GCGACGTCATGACTCCGAGCTCAAGCTCAGGCGTAACCAACC	61 ATTGCAACAACAACGACACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA 1020	-	21 GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACACTGA 1071%	-
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e 1034, Application US/09938842A tion No. US20040009476A9

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APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF FLANTS, TRANSGENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME; AND METHODS OF USE
FILE REPERRECE: SCRIP1300-3
CURRENT APPLICATION NUMBER: US/09/936,842A
CURRENT FILING DATE: 2001-01-08-24
FRIOR APPLICATION NUMBER: US 60/227,866
PRIOR PLING DATE: 2000-08-24
PRIOR PLING DATE: 2000-08-24
PRIOR PLING DATE: 2001-01-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                361 AACGCTGAGCCGGCGATTATAGCCGCCACGGTACGGGAACGGTTCCCGCCATCGCCATG 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              421 TCGGTTAACGGAACCTTAAAATCCCCGACGACGACGAACGCTGATTCTGATATGGGTGAA 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 12, Length 1071
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 1071;
Best Local Similarity 100.0%; Pred. No. 0,
Matches 1071; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            dopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                          ) TYPE: DNA
) ORGANISM: Arabi
US-09-938-842A-1034
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900 AGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTC 959
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IIILE OF INVENTION: Expressed Sequences of Arabidopsis
IIILE OF INVENTION: thaliana
FILE REFERENCE: 2027 (PARA-016PRV)
CURRENT PEDLICATION NUMBER: US/09/770,444
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: 60/178,502
PRIOR APPLICATION NUMBER: 60/178,502
NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastsEQ for Windows Version 4.0
SEQ ID NO 615
LUNCTH: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
41.0%; Score 439; DB 9; Length 453
Best Local Similarity 99.1%; Pred. No. 1,1e-141;
Matches 450; Conservative 0; Mismatches 3; Indels
                                                                                                                                                                                                                      41 AGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1
                                                                                                                                                                                                                                                                                                                                                          Sequence 615, Application US/09770444
Patent No. US2002023280Al
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Arabidopsis thaliana FEATURE:
NAME/KEY: misc feature
NOCATION: (1)...(453)
OTHER INFORMATION: n = A.T.C or GUS-09-770-444-615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yu, Yang
Pancaka, Joshua G.
Page, Amy
Matthew, Abraham V.
Ledford, Brooke L.
Woesener, Jeffer L.
Haas, William David
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LICANT: Gorlach, Jorn
LICANT: An, Yong-Qiang
LICANT: Hamilton, Carol M.
LICANT: Price, Jennifer L.
LICANT: Raines, Tracy M.
                                                                                                                                                                                       1020 AGAGCT
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                                                                                                     781 TCGTCTTACGTCGCCGCTGTTCAACAGCTTCCACGATGCCTAGACCACCTCCTTTACAA 840
                                                                                                                                                              GTIGITCCAAGCAGCGGCTTTGTAICCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGA 900
                                                                                                                                                                                                      841 Gridriccaagcagcarriciariccerricagaccriagcagricgaarriarcaaga 900
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41.8%; Score 448; DB 10; Length 460;
Best Local Similarity 99.6%; Pred. No. 8e-145;
Matches 459; Conservative 0; Mismatches 1; Indels
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LOCATION: (1)...(460)
OTHER INFORMATION: n = A,T,C or G
IS-09-924-035A-502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .09-924-035A-502/c
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960 AATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACA 1019
453 CTGGCATCCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATGTGGGCT 394
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                                                                                                                                                                                101 AATTIGCAACAACAACGCACACGCTGAGAGACTICTCCCTAGAGATAIACGAGAAACA 42
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121 TGATGCCGTCGTTTTCAATGTCTTTAGCTCCACCGTCTTCGACAGGACCACCATTGAAGA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATION NUMBER: US/09/934, 455
                                                                                                                                                                                                                                                              Application US/09934455
o. US20030121070A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: MBI 0022
PRIOR FILING DATE: 2001.11.16
PRIOR APPLICATION NUMBER: MBI 0023
PRIOR FILING DATE: 2001.04-17
NUMBER OF SEQ ID NOS: 516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 71.0°
Matches 171, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | FRATURE: CDS | NAME/KEY: CDS | LOCATION: (106)...(1575) | OTHER INFORMATION: G1064 | US-09-934-455-169
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ineda, Omair
                                                       215 GAGCT 219
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Reuber,
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                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 60/310,847
PRIOR FILING DATE: 2001-08-09
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PSELSEQ for Windows Version 4.0
SEQ ID NO 165
LENGTH: 1728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12.0%; Score 129;
llarity 71.0%; Pred. No. 2
Conservative 0; Mismatch
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CURRENT APPLICATION NUMBER: US/10/225,068
CURRENT FILING DATE: 2002.00
                                                                   Mendel Biotechnology, Inc.
Application US/10225068
o. US20030217383A1
                                                                                                                                    Heard, Jacqueline E
Jiang, Cai-Zhong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                               Adam, Luc J.
Dubell, Arnold T.
Ratcliffe, Oliver
Pineda, Omaira
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APPLICANT: Creelman, Robert
                                                                                                                                                                                                                                                                        'u, Guo-Liang
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LOCATION: (106)...(1575)
IS-10-225-068-165
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Best Local Similarity
Matches 171; Conserv
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299 CGGATCCGTATGCCTGCCATGTGTGTGCTGCACGTGTCTTTCAGCTCACACGTGAGCTTGGT 358
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            APPLICANT: Richmann, Jose Luis
APPLICANT: Fichmann, Jose Luis
APPLICANT: Yu, Guo-Liang
APPLICANT: Pinded, Comaira
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
TITLE OF INVENTION: Genes for Modifying Plant Traits IV
CURRENT APPLICATION NUMBER: US/09/934,455
CURRENT FILING DATE: 2001-08-22
PRIOR FILING DATE: 2000-08-22
PRIOR PLILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR APPLICATION NUMBER: MBI-0023
PRIOR PLILING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 11.6%; Score 124.6; DB 11; Length Best Local Similarity 65.0%; Pred. No. 6.5e-32; Matches 184; Conservative 0; Mismatches 99; Indels
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o. US20030229915A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
CORGANISM: Arabidopsis thaliana
FEATURE:
MANE/KEY: CDS
LOCATION: (107)..(1084)
COTHER INFORMATION: G805
US-09-934-455-137
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Fromm, Michael
Heard, Jacqueline
Riechmann, Jose Luis
Lynne
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u, Guo-Liang
iang, Cai-Zh
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Pilgrim, Mare
Creelman, Rol
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0; Mismatches
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Pred. No. 6.5
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Riechmann, Jose Luis
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Similarity 65.0%;
84; Conservative
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u, Guo-Liang
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Reuber, Lynne
Jiang, Cai-Zhong
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roun, Pierre
      Yu, Guo-Liang
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; LOCATION: (107)...(1084)
US-10-225-068-245
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hang, James
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Best Local Simi.
Matches 184; (
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CURRENT FILIN
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Pred. No. 6.5e-32;
0; Mismatches 99;
PLANT GENE SEQUENCES II
                                       JRRENT APPLICATION NUMBER: US/10/302,267
                                                                         PRIOR APPLICATION NUMBER: US/09/506,720
PRIOR FILING DATE: 2000-02-17
PRIOR PPLICATION NUMBER: 60/120,880
PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: 60/121,037
                                                                                                                                    PRIOR FILING DATE: 1999-02-18
PRIOR APPLICATION WUMBER: 60/121,037
PRIOR FILING DATE: 1999-02-22
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-11
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-03-13
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/139,450
PRIOR APPLICATION NUMBER: 60/139,450
PRIOR APPLICATION NUMBER: 60/135,134
PRIOR APPLICATION NUMBER: 60/144,153
PRIOR FILING DATE: 1999-07-15
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PRIOR APPLICATION NUMBER: 60/162,656
PRIOR FILING DATE: 1999-11-01
                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/161,143
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, US20030217383A1
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iechmann, Jose Luis
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fiang, Cai-Zhong
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ORGANISM: Arabidopsis thallana
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Best Local Similarity 65.0%;
Matches 184; Conservative
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SOFTWARE: PatentIn Ver. 2
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LENGTH: 1231
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239 CCTCCTCCTAAACGAACCTCTACTAAAGACGACACAACAAAGTCGAAGGCCGAGGCCGT 298
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es 99; Indels
APPLICANT: Broun, Pierre E.
TITLE OF INVENTION: STRESS-RELATED POLYNUCLEOTIDES AND
TITLE OF INVENTION: POLYPEPTIDES IN PLANTS
FILE REPERENCE: 514442002040
CURRENT PELLING DATE: 2002-08-09
PRIOR APPLICATION NUMBER: 05/30,049
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR APPLICATION NUMBER: 60/336,049
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR FILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2001-11-19
PRIOR PILING DATE: 2002-06-14
NUMBER: 0F SEQ ID NOS: 246
SOFTWARE: PASLEEQ for Windows Version 4.0
SEQ ID NO 245
LENGTH: 1231
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NUMBER OF SEQ ID NOS: 999
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 675
LENGTH: 490
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CURRENT FILING DATE: 2001-08-22
  CURRENT APPLICATION NUMBER: US/09/770,961
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PRIOR PLING DATE: 2000-08-22
PRIOR APPLICATION NUMBER: MBI-0022
PRIOR FILING DATE: 2001-11-16
PRIOR PELING DATE: 2001-11-16
PRIOR PELING DATE: 2001-04-17
NUMBER OF SEQ ID NOS: 516
SOFTWARE: PREENTIN VERSION 3.1
LENGTH: 1009
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5. US20030121070A1
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NAME/KEY: misc_feature LOCATION: (1)...(490)
OCHER INFORMATION: n = A,T,C or G
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Pilgrim, Marsha
Ratcliffe, Oliver
Ruber, Lynne
Riechmann, Jose Luis
Yu, Guo-Liang
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                         CURRENT FILING DATE: 2001-01
PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 2000-01-27
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NAME/KEY: CDS
LOCATION: (27)
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                                   PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-10-06
PRIOR PELING DATE: 1998-11-17
PRIOR PELING DATE: 1998-11-17
PRIOR PELING DATE: 1998-11-17
PRIOR PELING DATE: 1998-11-22
NUMBER OF SEQ ID NOS: 170
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
SOFTWARE: Patentin Ver. 2.0
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. US20030115639A1
                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Arabidopsis thaliana
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Hamilton, Carol M.
Price, Jennifer L.
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meaka, Joshua G
FILING DATE: 1999-09-13
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LOCATION: (143)..(1345);
OTHER INFORMATION: G802
JS-10-295-403-147
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271 ATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAATCC 330
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                                                             Gaps
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0
   Length 490;
                                                          55; Indels
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Query Match
Best Local Similarity 73.3%; Pred. No. 7.2e-30;
Matches 151; Conservative 0; Mismatches 55;
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163 GTATGCCAATCATTTGCGCAGCTCGAGTTTTTCAATTGACCAGAGAGTTAGGTCACAAGT 222
                                                                                        329 CCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGCGATTATAGCCGCCA 388
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Pred. No. 2.7e-27;
0; Mismatches 58; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT PILING DATE: 2002-11-15
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FLING DATE: 1999-09-13
PRIOR FLING DATE: 1998-09-13
PRIOR FLING DATE: 1998-10-06
PRIOR FILING DATE: 1998-10-06
PRIOR FILING DATE: 1998-11-17
PRIOR PRIOR DATE: 1998-11-17
PRIOR PRIOR DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-17
SEQ ID NO 145
LENGTH: 1009
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FITLE OF INVENTION: PLANT GENE SEQUENCES I
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Riechmann, Jose Luis
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Best Local Similarity 71.6%;
Matches 146; Conservative
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u, Guo-Liang
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Jiang, Cai-Zhong
Keddie, James
Zhang, James
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; OTHER INFORMATION: G801
US-10-295-403-145
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LOCATION: (27)
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APPLICANT: Rechmann, Jose Luis
APPLICANT: Heard, Jacqueline E.
APPLICANT: Hang, Cal-Jang
APPLICANT: Jang, Cal-Jang
APPLICANT: Dubell, Arnold T.
APPLICANT: Pineda, Omaira
APPLICANT: Pineda, Omaira
APPLICANT: Puneda, Omaira
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0; Mismatches
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10.4%; Score 111.2; 1
Best Local Similarity 71.6%; Pred. No. 2.7e
Matches 146; Conservative 0; Mismatches
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NUMBER OF SEQ ID NOS: 246
SOFTWARE: FastSEQ for Windows Version 4.0
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PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/338,692
PRIOR FILING DATE: 2001-12-11
PRIOR APPLICATION NUMBER: 10/171,468
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IOR APPLICATION NUMBER: 60/310,847
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ORGANISM: Arabidopsis thaliana
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Matches 146; Conservative
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; OTHER INFORMATION: G801
US-09-934-455-133
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; NAME/KEY: CDS
; LOCATION: (27)...(746)
US-10-225-068-135
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162

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283 CTGGAACTGGCACTACTCCGGCGA 306

Search completed: February 2, 2004, 01:10:23 Job time : 414.599 secs

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Fax: 301-638-0208
Email: cdtown@tigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TF
Class: sheared ends.
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AV825375 AV825375
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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eudicots; rosids
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosid; eurosids II; Brassicales; Brassicaces; Arabidopsis.

(bases 1 to 486)
Seki, M., Narusaka, M., Ishida, J., Kamiya, A.; Satou, M., Nakajima, M., Oono, Y., Sakurai, T., Carninci, P., Kawai, J., Itoh, M., Ishii, Y., Arakawa, T., Saburai, T., Shinagawa, A., Muramatsu, M., Hayashizaki, Y. and Shinozaki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                  Email: mseki@rtc.riken.go.jp
Arabidopsis full-length conA library was constructed essentially
as reported previously (Seki et al., 1998).cDNA cleaved with BamHI
and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et
al., submitted for publication) digested with BamHI and SalI. This
clone is in a modified pBluescript vector. Please visit our web
site (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further
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/db xrefe="taxon:3702"
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/dev_stage="rosette plants"
/lab_host="nbH10"
/clone="lib="RAB17"
/nofc=="site 1: BamH1; Site 2: Sal1; subjected to
cold-treated (1, 2, 5, 10, 24 hr)"
31 a 118 c 117 g 117 t 3 others
                                                                                                                                                                                  Large scale analysis of Arabidopsis full-length cDNA (2002b)
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                                                                                                                                                                                                                                              Contact: Motoaki Seki
Plant Functional Genomics Research Group
RIKEN Genomics Center
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-4159
Fax: 81-298-36-815
Email: msekiertc.riken.go.jp
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Pred. No. 8.4e-110;
0; Mismatches 3;
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  Location/Qualifiers

1. 798

(organism="Brassica oleracea"
/mol type="genomic DNA"
/strain="TO100DH3"
/db_xref="taxon:3712"
/clone="ROHGA14"
/clone="Lib="BOHG4"
/clone="Tocot: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"

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/strain="var columbia"
/db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 517-353-0854
Fax: 517-353-9168
Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer.
Location/Qualifiers
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1 (Dases 1 to 373)
White,J.A., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
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Dept. of Bacochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               534 AAGCGACGCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGATGCCA 593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     594 ACCTCCGCAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTA 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            130 TCCGATGTGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGAT 189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCCACAAATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTTCCCGCCGCCGCTGC 773
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany
Zoology Bldg., 1735 Neil.Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 AGGGGACGCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAACGATGCA 69
                                                                                                                                                                                                                  nurte, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C. A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic pathway from carbohydrates to seed oil lant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Arabidopsis developing seed"
/notes="Organ: Developing seed; Vector: pBluescript SK-;
Site_l: EcoRl; Site_2: Xholl"
118 c 82 g 100 t
M28F8STM Arabidopsis developing seed Arabidopsis thaliana CDNA clone M28F8 5', mRNA sequence.
BE522768
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 360.8; DB 10; Length
Pred. No. 4e-103;
0; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tissue type="seed"
dev_stage="5-13 days after flowering"
lab_host="E.coli"
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clone="M28F8"
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strain="Columbia"
                                                                          BE522768.1 GI:9780746
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Best Local Similarity 99.5%;
Matches 362; Conservative
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1 (bases 1 to 335)
Newman, T. deBruijn, F.J., Green, P., Keegstra, K., Kerde, H., McIntosh, N., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, B. and Somerville, C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis CDNA clones Plant Physiol. 106, 1241-1255 (1994)
EST 09-JAN-1998
                                                                                                                                                                                                                                                                                                            Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta, Magnollophyta, eudicocyledons, Core eudicots, rosids;
seurosids II, Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 335)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          61 TCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAATCC 120
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335 bp mRNA linear EST 09-JAN-1
12149 Lambda-PRL2 Arabidopsis thaliana cDNA clone 156J1T7, mRNA
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MSU-DOB-PRL, Michigan State University, Plant Biology Bldg., E
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Contact: Thomas Newman
MSU-DOB Plant Research Laboratory
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o O	CACAGIGAGICICGAGCCCAAGGCGGACGININNAIGCCGICNITITCAAIGINTITAGC 18		TGACGTGGCGGAAAATCCGGCGAAGAAGAGACGTAAGGGACCTTCTACCAGTGAGTATAT
ò	183 TCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGTCACACGA 242	ò	528 AGACATAAGCGACGCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAAC 587
OD	181 recaceginitedacadadaccaecatigaagageritegaciaaaagacegicacadaaa 240	4 du	417 AGACATAAACGAACCGGTCTCCGTTTCCTCCGGTTTAGCTCC376
Qy Db	243 GGTTGAAGGAAGAAGAAGAATACGGATGCCTGCCACCTGTGCGGCTAGGATTTTCA 302 241 GGTTGAAGGAAGAGGAAGAAGATACGGATGCCTGNNACGTNTGCGGCTAGGATTTTNCA 300	Oy 00	588 GATCCAACCTCCGCAAGCTCTGGCATCATCCACTGTGGCTCACCACCACTTCTGCCGCAAGG 647 375GGCATCCACCGCGGGTCAAAACGCTGCCGCAGG 340
Oy Db	ATTAACTCGAGAGTTAGGTCACAATCCGACGGCG 337 		
RESULT 5 BH450567/c LOCUS DEFINITION	C BH4S0567 656 bp DNA linear GSS 12-DEC-2001 N BOGD041TR BOGD Brassica cleracea genomic clone BOGD041, genomic	, da 9	708 CTTGATTCCACAAATGGCTGGTCGAATGAGCCTCAGTTATTAGCTTTTCCCGC 764
ACCESSION VERSION KEYWORDS SOURCE OPCENTEM	survey sequence. BH450567.1 GI:17636278 GSS. Brassica oleracea		
CKGAN1SM REFERENCE AUTHORS TITLE	<pre>sn brassica Oleracea</pre>	RESULT 6 235068 LOCUS DEFINITION	235068 Gif-
¥	Unpublished Other GSSs: BOGDQ41TF Contact: Chris Town	ACCESSION VERSION	G1:510816
	11GK 9712 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-3523 Fax: 301-838-0208 Email: cdcown@tigr.org DNA is from a doubled haploid provided by Tom Osborn. Seg primer: TR	SCHWOLDS SCHRCE ONGANISM REFERENCE	AST. Arabidopsis thaliana Arabidopsis thaliana Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids ; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
FEATURES Sourc	<pre>Class: sheared ends. Location/Qualifiers ce</pre>	AUTHORS TITLE JOURNAL COMMENT	CNRS. The Arabidopsis thaliana transcribed genome: the GDR cDNA program Unpublished Berthomieu P., Guerrier D., Giraudat J. Genetique Moleculaire d'Arabidopsis
BASE COUNT	142 8	FEATURES	ISV - UPR40, CNRS Avenue de la Terrasse, 1198 Gif-sur-Yvette Cedex, France Email: Giraudat@cnrs-gif.fr. Location/Qualifiers 1. 388 /organism="Arabidopsis thaliana" /mol_type="mRNA" /db xref="taxon:3702"
Query Match Best Local S Matches 431	atch 29.1%; Score 311.2; DB 28; Length 656; cal Similarity 78.4%; Pred. No. 3.2e-87; 431; Conservative 0; Mismatches 73; Indels 46; Gaps 3;		/clone_nray344" /clone_lib="Gif-SeedA" /note="Tector: Lambda ZAPII non-oriented; Physiological /note="Tector: Lambda ZaPII non-oriented; Physiological condition: greenhouse plants. tissue_type: Green siliques
강 임	288 GGCTAGGATTITICAATTAACTGGAGAGTTAGGTCACAAATCCGACGGGAAAGGATTGG 347 	BASE COUNT ORIGIN	102 a 94 c 108 g 83 t 1 others
Qy Dp	348 GTGGTTGTTGGAGAAACGCTGAGCCGCGATTATAGCCGCCACGGGTACGGGAACGGTTCC 407	Query Match Best Local Matches 31	h Similarity 97.8%; Score 292.6; DB 14; Length 388; Similarity 97.8%; Pred. No. 1.9e-81; 17; Conservative 0; Mismatches 5; Indels 2; Gaps
۶۶ ج د	408 CGCCATCGCCATGTCGGTTAACGGAACCTTAAAAATCCCGACGACGACGACGACGATC 467	& &	86 GAAAGGTCGAAACTTCAAGACTTTCCAAGTAATCCCACAGTGAGTCTCCAGGCCCAAGG 145 
	TGATATGGGTGAAAATCTGATGAAGAAAGAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACGTAAACAGTAAATTATAAACGTAAACGTAAACGTAAACGTAAACAGTAAATTATAAACGTAAACGTAAACGTAAACGTAAACAGTAAATATAAACGTAAACGTAAACGTAAACAGTAAAATAAACGTAAACGTAAACGTAAACAGTAAAAAAAA		146 CGGAGCCGGTGATGCCGTTTTCAATGTCTTTAGCTCCACCGTCTTCGACAGGACCAC 205

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103 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT
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/organism="Brassica_oleracea"
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Contact: Chris Town
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Best Local Similarity 73.9
Matches 309; Conservative
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AUTHORS
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BH543331
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Spermatophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplana,
Bukaryota; Viridiplana,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
Spermatophyta; Magnoliophyta; Brassicaceae; Arabidopsis.

1 (Bases I to 378)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de Ilarduya, C., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing seeds. The metabolic palmay from carbohydrates to seed oil plant Physiol. 124 (4), 1582-1594 (2000)
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Fax: 517 353 9334

Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Onio State University, 309 Botany & Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX: 6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                    BE523004
378 bp mRNA linear EST 19-MAR-2001
3186STM Arabidopsis developing seed Arabidopsis thallana cDNA
clone M31B6 5', mRNA sequence.
BE523004
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                                                       TACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACA 325
                                                                                                                                                                       AATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGAACGCTGAGCCGGGGGATTA-TAGCC 384
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/dev_stage="5-13 days after flowering"
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/clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: pBluescript SK-;
site_l: EcoRl; Site_2: XhoII"
97 c 81 g 92 t
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Pred. No. 1.5e-69;
0; Mismatches 13; 1
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organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                     300 GCCACGGGTACGGGAACGGTTTCC 323
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strain="Columbia"
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Best Local Similarity 95.3%;
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Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 725)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Whole genome shotgun sequencing of Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BHS43331 725 bp DNA linear GSS 14-DEC-2001
BOGCN02TF BOGC Brassica oleracea genomic clone BOGCN02, genomic
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                                                             222
                                                                                                                                                                                                                                                                                                                                       283 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGGGGCTTCGACTAAAGACCGTCACACG 342
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GATCTAACCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
                                GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
                                                                                                                                    CCCACAGTGAGTCTCGAGGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA
                                                                                                                                                                                                  223 cccacagraarcrogagcccaaggcggagccgagcggraargccgrcgrrrrcaargrcrrra
                                                                                                                                                                                                                                                                      GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACCGTCACAG
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/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
198 c 191 g 154 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: 301-838-3523
Fax: 301-838-0208
Email: cdrowmetigr.org
DNA is from a doubled haploid provided by Tom Osborn.
Seq.primer: TF
Class: sheared ends.
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                                                                                                                                                                                                                                                                                                                                                                                                       241 AAGGITGAAGGAAGAGGAGAAGGATACGGATGCCT 276
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145 ACCGOTROCOTRICOTROCOTRINGCO-ACCASAMENTOCONAGONAMENTOCON 650 CCAAGOTROCOTROCOTROCOTROCOTROCOTROCOTROCOTRO	571	655 CCGAIGTGGGCTATICCAICAAACGCAAIGAITCCGACGGTCGGAGCTITCTTCTTGAIT 714	715 CCACAAATCGCTGGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGT 771	772 GCTTCGCCGTCGTCGTACGTGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCT 831	832 CCT 834       350 CCT 348	CB292965 LOCUS CB292965 LOCUS CB292965 DEFINITION UCRCS01 05bd03 g1 Washington Navel orange cold acclimated flavedo & albedo CDNA library Citrus sinensis cDNA clone UCRCS01_05bd03, mRNA sequence.	ACCESSION CE292965 CERSION CE392965.1 GI:28618422 KEYWORDS EST. SOURCE Citrus sinensis ORGANISM Citrus sinensis Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Sexmatophyta, Mannoliophyta, eudicotvledons, core eudicots, rosids	sids II; Sapindales; Rutaceae; Citrus. ses 1 to 791) T.J., Collurk, Fenton,R.D., Feuerbacher,O. p., Wanmaker,S., Wing,R. and Yu,Y.	COMMENT Unpublished COMMENT Contact: Timothy Close COMMENT Department of Botany & Plant Sciences, University of California Riverside, CA 92521-0124	Fax: 907/874310 Fax: 909/874431 Fax: 909/874431 Email: timothy.close@ucr.edu Seg primer: T3. FEATURES Location/Qualifiers	<pre>source 1. 791 /organism="Citrus sinensis" /mol_type="mRNA" /cultivar="Washington Navel" /db_xref="taxon:2711" /clone="UCRCSOL" /clone="UCRCSOL"</pre>	/tissue_type="Rind containing flavedo and albedo" /dev stage="Mature fruit" /lab_host="E. coll TJC11" /clone_lib="Washington Navel orange cold acclimated flavedo & albedo cDNA library".	/note="vector: Lambata Uni-Zay Kk, excised pagemila; Site 1: EcoRI; Site 2: XhoI; Plants were grown in the field at University of California, Riverside Agricultural Operations since 1981. The scion was Washington Navel orange and the roctetock Carizzo Citrange. Tissue from	mature fruit was harvested at mid-day in January 2002 during a cold spell, when pre-dawn temperatures were approximately -2 to 2 degree C. Approximately 2 m median serrions of the rind were excised in the field from	several fruits, then wrapped in aluminum foil and frozen quickly in dry ice. Total RNA was extracted using a phenol extraction procedure described in J. Japanaese Soc. Hort. Sci. (1995) 64:809-814. Polv(A) RNA was purified, a cDNA	library was made, and 1 million primary lambda cDNA clones were in vivo excised to give a population of pBluescript
145 ACCGCTCTCCGCATTAGGTC.  10 CAAGCTCTGGCATCACCACGCGCACCACACACACACTAGAA  10 CAAGCTCTGGCATCACCACCACGCGCACACACACACACAC	q	& <del>8</del>	<b>상</b> 옵	& B	& 43	N COR	SON KEE	K K	50	F						
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буно кнока бо р де	ACCGGTCTCCGGTTTTAGCTC	GCAAGCTCTGGGATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT	GTGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACACTTCTTCTTCTTCAAACACAAAAAGCAGGGGGGGG	AATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTC		BH470366 680 bp DNA linear GSS 1 BOH0133TF BOHC Brassica oleracea genomic clone BOHCI33, BH470366	BH470366.1 GI:17678477 GSS. Brassica oleracea I Brassica oleracea Elkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheop Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids II; Brassicales; Brassicaceae;	1 (bases 1 to 680) Town,C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,Whole genome shotgun sequencing of Brassica oleracea Unpublished Other_GSSs: BOHCI33TR	Contact: Chris lown TIGS 7122 Medical Center Drive, Rockville, MD 20850, USA. Tel: 301-838-1228 Fax: 301-838-0208	bilail: Cucomiecigi.cig DNA is from a doubled haploid provided by Seq primer: TF Class: sheared ends. Location/Qualifiers	e 1680 /organism="Brassica oleracea /mol_type="genomic DNA" /strain="TO100DH3" /db_xref="taxon:3712" /clone="BOHC13"	/clone_lib="BOHC" /note="Vector: pHOS1; Site_1: BstXI; 2-3 kb she genomic_DNA inserted into pHOS1 using BstXI lin 145 a 188 c. 175 g 172 t	15.4%; Score 165; DB 28; Length 680; imilarity 72.5%; Pred. No. 9.5e-41; ; Conservative 0; Mismatches 55; Indels 45; Gaps	GACATA        GACATA	agcgacggtttcagcttcctccggtttagctccaattgccacgacgacgatccaa 	CCTCCGCAAGCTCTGGCATCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTAT

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AW697442
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Best Local Simi
Matches 195;
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SK(-) phagemids. All steps to this point were performed in the TU Close lab at the University of California, Riverside (Fenton). Phagemids were plated, plasmid DNA purified, cDNA clones archived, and DNA sequences determined bi-directionally using an AB1350 at the Arizona Genomics Institute, University of Arizona (Collura , Feuerbacher, Kim, Kudrna, Wing, Yu). Chromatogram files were transmitted to UC Riverside (by Yu), then processed at UC Riverside (by Wanmanker) using the HarvEST pipeline (http://harvest.uor.edu) to remove vector and cloning oligo sequences and various contaminants, and to trim to a high quality region of at least 100 bases were deposited to GenBank."
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AU239448 RAFL19 Arabidopsis thaliana cDNA clone RAFL19-81-E01 5',
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Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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An Arabidopsis full-length cDNA library was constructed essentially
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Large scale analysis of Arabidopsis full-length cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAATCCGAC 333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        296 TCTCCAGCGAAACCTG---CCGGCGAAGAACTGCCGAGGAAACGGCGGAAGAGACCGTGT 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         454 ACGAACGCTGATTCTGATATGGGTGAAAATCTGATGAAGAAGAAGGTAAACGACCTTCT
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Pred. No. 1.6e-40;
0; Mismatches 91; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               514 AACAGTGAGTATATAGACATAAGCGA 539
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as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further details.
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NF118G06ST1F1051 Developing stem Medicago truncatula cDNA clone
NF118G06ST 5', mRNA sequence.
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X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel
.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     255 AGGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGA
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/ organism="Arabidopsis thaliana"
/ mol type="mRNR"
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/ clone="RRALID=81.E01"
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Plant Biology Division
The Samuel Roberts Noble Foundation
1510 Sam Noble Parkway, Ardmore, OK
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Insert Length: 652 Std
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Fax: 580 221 7380
Email: radixon@nob
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
asterids, campanulids, Asterales, Asteraceae, Cichorioideae,
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1 (bases 1 to 747)

Lin,H., wan Damme,M., Lavelle,D., Chevalier,P., Ziegle,J., Ellison,P., Kolkman,J., Slabaugh,M.S., Livingston,K., Zhou,Y., Lai,Z., F., Kolkman,J., Jackson,L., and Bradford,K.

Lettuce and Sunflower ESTs from the Compositae Genome Project http://compgenomics.ucdavis.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         255 AAATCAGACGGTGAAACCGTTAGATGGCTGCTTGAACATGCTGAGGAAGCTATTATTGAA 196
                                                                                                                                                                                                                                           435 GCTATGCAGATGCAGACGCCAATGCCAATTTCAATGCCTCTGCCAGTCACTACAACAGCA 376
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Department of Vegetable Crops, R.W.Michelmore Lab
University of California at Davis (UCD)
Asmundson Hall, UCD, Davis, CA 95616, USA
Tel: 1-(530)-742-1742
Fax: 1-(530)-752-659
Email: akozik@atgc.org [michelmore@vegmail.ucdavis.edu]
singleton, see http://cggdb.ucdavis.edu/ for details.
Plate: QCS row: H column: 15.
Dication/Qualifiers
                                                                                                     Score 149.2; DB 14; Length
Pred. No. 7.9e-36;
0; Mismatches 153; Indels
                                  124
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/mol_type="mRNA"
/cultivar="Salinas"
       /note="Organ: apex"
98 c 126 g
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Matches 254; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Populus tremuloides (quaking aspen)
Populus tremuloides
Populus tremuloides
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, agnoliophyta; eudicotyledons, core eudicots, rosids
; eurosids I; Malpighiales, Salicaceae; Populus.
1 (bases 1 to 439)
Ranjan, P., Kao, Y.-Y., Harding, S.A., Jiang, H., Joshi, C.P. and Tsai
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EST 30-DEC-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  228 AGCTCAAGCTCAAGCCCAACAATTCAAAAGAGATCATCTACAAAAGACCGTCACAC 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240 GAAGGITGAAGGAAGAGGAAGAAAGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            300 TCAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             288 AAAAGICGAGGGTCGAGGCCGAAGGAICCGAAIGCCIGCCACAIGIGCAGCICGGAICTI 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         360 GAACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCAT 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  408 ACACGCGGAGCCAGCTATCATTGCCGCCACCGGTACGGCACAGTCCGAGCCATCGCCAT 467
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 AGCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACCGTCACAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     439 bp mRNA linear EST 30-DEC. MTU2CA.P4.C10 Aspen apex cDNA Library Populus tremuloides cDNA CA929907
                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Tsai C-J
Plant Biotech Research Center
Michigan Technological University, School of Forest Resources
Environmental Science
1400 Townsend Drive, Houghton, MI 49931-1295, USA
Tel: 906 487 2914
Fax: 906 487 2915
                                                                                         /organism="Medicago truncatula"
/organism="MRAM"
/mol type="MRAM"
/mol type="MRAM"
/db yref="trans.1386"
/clone="NF118G06ST"
/tissue type="stem"
/day stage="Pooled davelopmental"
/clone_11b="Developing stem"
/clone_11b="Developing stem"
/note="Vector: Lambda Zap; Contains a mixture of internoal stem segments"
/note="Vector: Lambda Zap; Contains a mixture of internoal stem segments"
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                                                                                                                                                                                                                                                                                                                                                                                 Length 652;
                                                                                                                                                                                                                                                                                                                                                                              Score 154.6; DB 9; Length
Pred. No. 1.9e-37;
0; Mismatches 74; Indels
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/db_xref="taxon:3693"
/clone_lib="Aspen apex cDNA Library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                organism="Populus tremuloides"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 GTCGGTTAACGGAACCTTAAAAATCCCGACGAC 452
Plate: 118 row: G column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
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                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: chtsai@mtu.edu.
Location/Qualifiers
1. 439
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Best Local Similarity 72.9%;
Matches 199; Conservative
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CA929907/c
LOCUS
DEFINITION
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VERSION
KEYWORDS
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ORGANISM
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ORIGIN
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JOURNAL
JOMMENT
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                                                    FEATURES
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us-09-938-842a-1034.rst

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/clone_lib="Gm-closs" / folione_lib="Gm-closs"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 Gráckicháckáckáckáckárárararárkakárkákakáckickákákkakakakak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            569 ATTATTCGACGCACCGCCACGCCACGCTCCGGCCATCCGATCTCGGCCATTGGAACG 628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Gibcobri, This library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTCAATGTCTTTAGCTCCACCGTCTTCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    389 caggeccaaccacaaaagecggecriccaccaaagaccgccacacaagragagggggg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              256 GGGAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTCAATTAACTCGAGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="GENOME SYSTEMS CLONE ID: Gm-c1053-1227"
/tissue_type="Whole seedling, 3 week old, greenhouse
Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone is available through: ResGen, Invitrogen Corp.

South Memorial Parkway Huntsville, AL 35801 For further if call: (800) -233-4363 or contact via email: ccu@resgen.com

Insert Length: 1706 Std Error: 0.00
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Pred. No. 1.2e-34;
0; Mismatches 107; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        organism="Glycine max"
                                                                                                                                                                                                                                                                                                                                   High quality sequence stop: 415
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'mol_type="mRNA"
'db_xref="taxon:3847"
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Best Local Similarity 66.2%;
Matches 210; Conservative
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Job time
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                                                                                                               /clone lib="0g ABCD1 lettuce salinas"
/clone lib="0g ABCD1 lettuce salinas"
/note="Vector: pBRcDNASfiAB; The library was constructed
from 10 different sources of RNA from a single genotype.
Separate cDNAs were generated using primers that
incorporated unique 5' and 3' tags to distinguish each
source of RNA. CDNAs were then pooled, size-fractionated,
directionally cloned into a custom medium-copy vector and
transformations made with four size classes to minimize
size blas. Details of each source of RNA and library
construction can be obtained at http://cgpdb.ucdavis.edu/
TAG_LIB=QG_ABCDI lettuce salinas
TAG_LIS=CG_ABCDI lettuce salinas
TAG_LIS=CG_ABCDI lettuce salinas
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/mol_type="genomic DNA"
/db_xref="taxon:3702"
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Patent: WO 0216655-A 1034 28-FEB-2002;
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Arabidopsis thaliana putative PCF2-like DNA binding protein
(At2g45680; F17K2.21) mRNA, complete cds.
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LEPKAEPVMPSFSKASLAPPSSTGPPLKRASTKDRHTKVBGRGRRIRMPATCAARIFOL
TRELGHKSDGBTIRWILENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTINADSDMGB
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PMMAIPSNAMIPTVGAFFLIPQIAGPSNQPQLLAPPAAAASPSSYVAAVQQASTMARP
PPLQVVPSSGFVSVSDVSGSNLSRATSVMAPSSSSGVTTGSSSSIATTTHTLRDFSL
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Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Magnollophyta, eudicotyledons, core eudicots;
rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
1 (bases 1 to 1071)
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Submitted (17-APR-2001) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
901 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA
                                                                                                                                                                                                                   961 ATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACAA
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This clone was isolated by RT-PCR.
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Best Local Similarity 100 0%; Pred. No. 0;
Matches 1071; Conservative 0; Mismatches 0;
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| db_xref="GI:13877695"
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/db_xref="taxon:3702"
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/db.xref="di1:21281085"
/translation="MATIOKLEEVAGKDOTLRAVDLTIINGVRNVETSRPFQVNPTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-NAY-2002) Plant Gene Expression Center, 800 Buchanan Street, Albany, Cas, 94710, USA
The RIEM Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL CDNA: 'RIKEN Arbidopes's Full-Length CDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai, J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                         ukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, permatophyta, Magnoliophyta, eudicotyledons, core eudicots, ostids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
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Arabidopsis thaliana putative PCF2 DNA binding protein (At2945680)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada, K., Banh, J., Chan, M.M., Chang, C. H., Chang, E., Dale, J. M., Deng, J. M., Goldsmith, A. D., Lee, J. M., Onodera, C. S., Quach, H. L., Tang, C. C., Toriumi, M., Wu, H. C., Yamamura, Y., Yu, G., Boweer, L., Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B. Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C. J., Sakurai, T. Bato, M., Schinn, P., Southwick, A., Shinozaki, K., Dake, Submission
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ann,G., Kim,C., Lam,B., Lin,J
., Shinn,P., Southwick,A.,
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ecotype: Columbia"
1. 1102
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Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
/chromosome="2"
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901 GCGACGTCGGTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTT 901 GCGACGTCGGTTATGGCTCCGAGCTCAGCGTAACCACCGGTAGTTC 1	DD 1021 GAGCTTCACCAGTTCATGAGCACCACAGCACCACTGA 1071  DD 1021 GAGCTTCACCAGTTCATGAGCACCACAGCACGCTCATCGAACCACTGA 1071  RESULT 4	AYOS ON Arab mRNA N AYOS AYOS	KEYWORDS FLI CDNA. SOURCE Arabidopsis thallana (thale cress) ORGANISM Arabidopsis thallana (thale cress) Bubaryota, Viridiplante, Streptophyta, Embryophyta, Tracheophyta; Spermacophyta, Magnollophyta, endicotyledons; core	rosids; Eurosids II; Brassicales; Brassicaceae, Arabidopsis. REPERENCE I (bases 1 to 1660) AUTHORS Yamada, K. Ilui, S.K., Sakano, H., Pham, P.K., Banh, J., Chung, M.K., Goldsmith, A.D., Lee, J.M., Ouach, H.L., Torium, M., Vi, G. Bowser, I.	Carninci, P., Chen, H., Cheu, R., Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B., Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Pah, C.G., Sakurai, T., Saturai, T., Saturai, T., Saturai, M., Satura	Davis, R.W., Scher, Sallar, S. Southard, A. Arabidopsis Full Length cDNA Clones Unpublished	AUTHORS Yamada.K. Banh J., Banno F., Dale, J.M., Goldsmith, A.D., Lee, J.M., Onodera, C.S., Quach, H.L., Tang, C.C., Toriumi, M., Yamamura, Y., Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R.,	dayashizaki, r., lshida, J., Jones, T., Kamiya, A., Kariin-Neumann, G., Kawai, J., Kim, C., Kossema, B., Lam, B., Lin, J., Meyers, M.C. Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T., Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S.E.,	Shinozaki,K., Davis,R.W., Ecker,J.R. and Theologis,A., Direct Submission [AL Submitted (12-SEP-2001) Plant Gene Expression Center, 8 Street, Albany, CA 94710, USA	COMMENT RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNA; "RIKEN Arabidopsis Full-Length CDNA"): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakural,T., Carninci,P., Kawai,J.,	inozaki,K. GEC (SSP) Consortium membe tion of the RAFL cDNAs: Ya	<pre>Banno,F., Dale,J.M., Goldsmith,A.D., Lee,J.M., Onodera,C.S., Ouach,H.L., Tang,C.C., Toriumi,M., Yamamura,Y., Yu,G., Yu,S., Bowser,L., Chen,H., Cheuk,R., Jones,T., Karlin-Neumann,G., Koesema,E., Lam,B., Lin,J., Meyers,M.C., Miranda,M., Nguyen,M.,</pre>	Sournw gis, A. and Se	Shinozaki, K. (RIKEN GSC) and dequally to this work as FIS. is based on the January 2002.	
LEPKAEPVWPSFSWSLAPPSSTGPPLKRASTKDRHTKVEGRGRRIBWPATCAARIFQL TRELGHKSDGETIFWLLENAEPAIIAATGTGTVPAIAMSVNGTLKIPTTTANDSDMGE NLMKKTRRKPSNSSYIDISDAVGASSGLAPIATTTTQPPQALASSTVAQQQLILPCGNY PNWAIPSNAMIPTVGAFFLIPQIAGPSNQPQLLAFPAAAASPSSYVAAVQQASTMARP PPLQVVPSSGFVSVSDSVSSNLSRATSVMAPSSSSGVTTGSSSSIATTTHTLRDFSL 3/UTR 10721102 BASE COUNT 300 a 291 c 267 g 244 t	Query Match Best Local Similarity 100.0%; Pred. No. 0; Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0; I ATGGGAGAATTGGAGGGGAAGATCAAAGGGGTA 60	1 ATGGCGACAATTCAGAAGCTTGAGAAGTTGCGAAAGTCAAACTTTAAGAGCCCTT 60. 61 GATCTAACCATCATCAAGGCGTCAGAAACTTGCAAAACTTCAAGACCTTTCCAAGTAAAT 120 61 GATCTAACCATCATCAAGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 120	CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGGGTGATGCCGTCTTTAATGTCTTTA	GCTCCACCGTCTT 		301 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 360 	361 AACGCTGAGCGGCGATTATAGCCGCCACGGGAACGGAAC	421 TCGGTTAACGGAACCTTAAAAATCCCGACGACGACGACGACGTGATTCTGATATGGGTGAA 480	481 AATCTGATGAAGAAAGGAAGACGTTCTAACAGTGAGTATATAGACATAAAGGGAC 540	541 GCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAACGATCCAACCTCCG 600	601 CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 660	661 IGGGCIATICCAICAAACGCAATGAITCCGACGGTCGGAGCTITCTICTICAIGAITCCACAA 720 	721 ATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCTGCTTCGCCG 780 721 ATCGCTGGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTCGCCG 780	781 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCTTTACAA 840 781 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCTTTACAA 840	<b>\$</b> =

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943 GITGITCCAAGCAGCGGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGA 1002
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Arabidopsis thaliana chromosome 2 BAC F17K2 genomic seguence,
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Bukaryota; Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis
1 (bases 1 to 91854)
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        643 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTTGCCACGACGACAACGATCCAACCTCCG 702
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3. (bases I to 91854)
Town, C.D. and Kaul, S.
Direct Submission
Submitted (12-F8B-2002) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598396.
Address all correspondence to:at@tigr.org
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The orientation of the sequence is from SP6 to 77 end of the BAC
                                                                                           TGGGCIATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTTCATTCCACAA
                                                                                                                                                                                           763 TGGGCTATTCCATCAAAGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAA
                                                                                                                                                                                                                                                                   ATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTTCCCGCCGCCGCTGCTTCGCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                /clone="RAFL07-08-P04 (R10678)"
/note="This clone is in a modified pBluescript vector (FLC-1) as a BamHI/XhoI insert.
ecotype: Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GATCTAACCATCATCAACGGGGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCCACAGTGAGTCTCGAGGCCGAAGGCGGAGCCGGTGATGCCGTTTTCAATGTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCCACAGTGACTCTCGAGCCCAAGGCGGAGCCGCTGATGCTTTTCAATGTCTTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATGGCGACAATTCAGAAGCTTGAAGAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCTAACCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAGACCGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTTCGACTAAAGACCGTCACACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGGTTGAAGGAAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCCGCCATG
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0
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/db_xref="taxon:3702"
/dbromosome="2"
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                                                                                                                                                                                                                                                                                                          103. .1173
/gene="At2g45680"
                                                                                                                                                                                                                               /gene="At2g45680"
1. .102
                                                                                                                                                                                                                                                                                   gene="At2g45680"
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Best Local Simi:
Matches 1071; (
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RIGIN
                                                                                                                                                                                                                                                        5'UTR
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us-09-938-842a-1034.oli.rge

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4092. .4215,4582. .4112,4769. .4864,4948. .5188,5352. .5374,
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                                                                                                                                                                                                                                                                                                              /trānglation="MSFLRGIIDSFSSILNEESKKDPSVSSSSTSSESMNGIDGVPVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESQATFRVVSASSLTSKWIDSIMSTRSTSENEASRRLKSEFLIQPDGVTSNPDDLVII
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRFIVESEKDPENMNDKYLRDIILNFMIAGKDTTAALLSWFLYMLCKNPLVQEKIVQE
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GPRICLGKDPAYRQMKIVSMALLHFPRFRMADENSKYYKRMITLHVDGGLHCAIFR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tränslation="MGGKGKKRREKNYLAAHGGPARLPPPPDRSKQDDVPSTLRILMN
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VVPKARKSTLSASQERLRLGAIDAYRSRKGWTARPGVPIPAVMQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHSSRENMADLLGHGI FAVDGEKARQRKLSSFEFSTRVLRDFSCSVFRRNASKLVOF
VSEFALSGKAFDAQDLLMRCTLDSI FKVGFGVELKCLDGFSKEGQEFMEAFDEGNVAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SSRFIDPLWKLKWFFNIGSQSKLKKSIATIDKFVYSLITTKRKELAKEQNTVVREDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(8412. .9632)
/gene="At2g45520"
/note="synonym: F17K2.5; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note="synonym: F17K2.6; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /noce="synonym: F17K2.4"

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8100. .8288)

/gene="ALS45510"

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Join(6429. .6950,7026. .7310,7386. .7724,7806. .8006,
9100. .8288)
19608-18c2945510"
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9289. .9356,9459. .>9632))
/gene="At2g45520"
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9289. .9356,9459. .9612))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /ccdon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /rpt_family="(CA)n"
complement(9578, .9632)
/rpt_family="(GA)n"
9822 10798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5429. .8288
/gene="At2g45510"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene="At2g45530"
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gene="At2g45530"
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http://ccR-081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant of GlimmerM, see Minaela Pertea.
http://www.tigr.org/softelab/glimmerm.html/glimmerm.html, and GeneSplicer (Wihaela Pertea and Steven Salzberg, contact mperteadrigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with BST similarity are named as unknown proteins. Genes without proteins over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by transcription programs over most of their length are annotated by transcription proteins. Genes encoding tRNAs are predicted by transcription proteins. Genes encoding tRNAs are predicted by Location proteins are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/Repeatmasker (Arian Smit, http.//ftp.genome.edu/RM/Repeatmasker 
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NGGLFHGIHFSPDTVLOERGCFELGYBTDBREGRENDGKKWRCHDLLSGKWRCN
KHWIRGMKKKHPVDTTNSHENAGFSPLTVETAAVRSVVPCKDGDDOKHSVSVMGITLPR
VSDKSTSSCSTDTTTDTALRGEDDDREYLSLFSPGV"
COMplement (1919. . . 2388)
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HGGELYGVLKQNGHLTEQQAATYIASLSQALAYCHGKCVIHRDIKPENLLLDHEGRLK
IADFGWSVQSSNKRKTMCGTLDYLAPEMVENRDHDYAVDNWTLGILCYEFLYGNPPFE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="DESKPSVQKFFPEVSDKCLEAAKFSSNRKNDIIARSREWKNMNV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="F17K2"
complement(1. .1281)
/note="overlap with BAC clone F4L23 (AC002387:1, .1281)."
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1655. .1750,1886. .2128,2260. .2388))
Genes Atcg45490"
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protein id="AAC06151.1"
db_xref="GI:2979542"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="genomic DNA"
cultivar="Columbia"
/db_xref="texon:3702"
/chromosome="2"
/map="CIC02E07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              'product="hypothetical protein"
'protein id="AAF18607.2"
db_xref="G1:20197053"
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oin(<57. .242,335. .>747)
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gene="At2g45480"
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/gene="At2g45500"
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oin(57. .242,33
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/clone="T1J8"
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complement(join(<10833. 11272,11438. 11560,11636. 12378,
12454. 12937,13953. 13119,13254. 13374,13464. 13548,
13645. 13794,13957. 144073,14178. 14264,14350. 145418,
14520. 14576,14730. 14813,14926. 14995,15396. 15538,
15768. 15244,16322. 16465,16545. 17093,17237. 17431,
17612. 17696,18015. 18613,18944. 19249,1963. 19914,
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         /trānslation="MOSSSSGGDDLEKOQOQOCKDKSPOKOSBSANESNHLTIVVCN
GDSSREELVGQIPPEKEVSLSRNGSSHEQCRVCLQDKEEVLIELGCQCRGGLAKAHRS
VAPSHTIGGLMSDNQCETCQVVANVYPPETQETTNYWWRIDDSYRQBERERGGFSPLW
VAPSILIGGLMSDNISITLGVSALPVNIIIGVIVVLGLGTALRLTLEFCYEWSLRRA
VHRAVQRAZANNFSNIAYPPAL"
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                                                                                                                       /rpt_family="(CAG)n"
complement(10833...25573)
/gene="At2g45540"
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Best Local Simil
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2 clone TlJ8 map 96825, complete
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                                                                                                                                                                                                                                                                                                                                                           GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA
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                                                                                                                                                                                                                                                    GTTGTTCCAAGCAGCGCTTTGTATCCGTTTCAGACGTTAGCGGTTCCAATTTATCAAGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin, X., Kaul, S., Shea, T. P., Fujii, C.Y., Shen, M., Vanaken, S.E., Barnstead, M.E., Mason, T. M., Bowman, C.L., Ronning, C.M., Benito, M.-I., Carrera, A.J., Creasy, T.H., Buell, C.R., Town, C.D., Nierman, W.C., Fraser, C.M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (right end) to position 181918 of our previous Phase II submission YUP8H12 accession number AC000098. This fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA 74061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GAGCTTCACCAGTTCATGAGCACCACACACACGGTCATCGAACCACTGA 1071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AC006922
Arabidopsis thaliana chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .134151
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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mRNA

CDS

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/gome="synonym: T108.5, similar to cellulase (xyloglucan endo transglycosylase) GI:311835 from (fropaeolum majus); supported by full length cDNA: Ceres: 7831" complement (join (<33824. 34414,35094. 35311,35394.
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TIKLGKNCEIDLFYVSDGRKILDSSKLALLITRLARLQOPLRVYMMRGPDTELLV
TNPVELSGKGRPQVFHDIALALKKIDTCIFSARIGRHVTGDREWBYYKVLINEDBDLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LVKADIHGKDEEIYSIKLPODPKLGEGKPENONHAIVFTRGEAICTIDKNQDNYLEEA
INGKNILLEEFHGKHGIRRPTILGVERHYFTGRYRMHYGHPDVFDRIFHITRGSISKAS
RVINISEDIXAGMRPNSTLENGANITHHEDVGLNQIALFEGKVAGGNGEQVLSRDVYRI
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IFTAVPMVMGFILELGLLKAIFSFITMQPQLCSVFFTFSLGTRTHYFGRILLHGGAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KGFRNLMGPQHQRMDQNALTIWLDRTSGSGFKSVRPFRSGYFGANITLQPGYYAGVIT
SLYLSNNEAHPGFHDEVDIEFLGTTFGKPYTLQTNYTRGSGDGKIIGREMKFRLWFD
PTKDFHHYAILWSPREIIFLVDDIPIRRYPKKSASTFPLRPMMLYGSIWDASSWATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKYKADYKYQPETAKYTNFKALGCTAYSSARCYFLSASPYRSGGLTRQQHQAKRWYQT
HAWYNYGCXCYKRHSLTFEECWR:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'translation="MGNSLISLLSIFHLLVLWGSSVNAYWPPSPGYWPSSKYGSLNFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GQQKQQKKPEATDIGLLLQRYEALRVAFIHSBDVGNGDGGSGGKKEFYSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(34048. .34414,35094. .35311,35394. .35494,
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18879. 18921,19083. 19201,19820. 19735,20017. 20136,

20301. 20424 20823. 20988,21079, 21147,21292. 21426,

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/product "puterive glucan synthase"

/product "puterive glucan synthase"
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'IPTGWALLSLAITWKQVIRVLGLWETVREFGRIYDAAMGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YLLLYIAMTVEDPEDWYSWLMYKGGYGYKGELSWESKWEEEGAHIOTIRGRILET
LRPFWFQYGIVYKLDLTRKKYTSLALXGYSWYYLVYIYFLFKGYASITFIALIYVA
TDLSIPDWFACVIGFIPTGWALLSLAITWKOYLRYLGLWETYREFGRIYDAAMGM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              product="xyloglucan endotransglycosylase, putative"
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LRSENEDGISILFYLQKIFPDEWENFLERIGRSESTGDADLQASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPIALLSWFPF1STFQSRLLFNQAFSRGLEISI ILAGNRANVET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product="ERNA-Tyr"
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complement (33824".35833)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               db_xref="GI:4883600"

'trānslation="MPIRNIAIGRPDEATRPDALKAALABFISTLIFVVAGSGSGMAF

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31LYWIAQLLGSVVACLILKFATGGLAVPAFCLSAGYGVLNRAVFEIVWTFGLVYTVY

na tidpkNGSLGTIAPIAIGFIVGANILAGGAFSGASMNPAVAFGPAVVSWTWTNHWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           omplement (join(<10803. .11068,11697. .11765,12150:3.12260,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="synonym: T1J8.2; predicted by genefinder;supported by tull length cDNA: Ceres:108427: complement(join(<12752.13150,13249. .13533,13650. [13971,14054. .14159,14237. .14464,14576. .>14806))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein id="AAM15323.1"

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Aranslation="WAKKGGATLAEDAPWRVSSGRPVPKISRSPVLSISQNPETDYAI

SVMKHPNPVGGGFAMEAVLESAGPBCVVPGQVTPLRLLGVKVWPVEVDLKFLEFVGKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement [join(13013. .13150,13249. .13533,13650. .13971,4054. .14159,14237. .14464,14576. .14729))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 codon start=1
product="putative aquaporin (tonoplast intrinsic protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        omplement (join(11018. .11068,11697. .11765,12150. .12260, 2343. .12466)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ="MGILSDDVVIISQSEKEGDPSVITINCPDKTGLGCDLCRILLFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLNIVRGDVSTDGKWCYLVFWVIGKPNTRWNLLKMRLVEASPSFSWAFGISRCYLSDS
ESQPPKLPDLFLKLACSDRTGLLYDVTBVLYKLBINIBKVKISTTPDGKVMDLFFVT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note="synonym: TlJ8.24; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="synonym: TlJ8.1; supported by full length cDNA:
eres:36633"
oin(6605. .7052,7144. .7737)
note="overlap with BAC clone F13K3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WAGPLVGGGIAGLIYEVFFINTTHEQLPTTDY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="molecular marker ve017"
oin(6669. 7052,7144. 7515)
gene="At2g36830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              oin(6605. .7052,7144. .7737)
gene="At2g36830"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               product="Expressed protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed protein"
d="AAD31570.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene="At2g36835" .12597)
note="at2g36835"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        JKMLGKFMDNAVELMNKSFIDR"
complement (12752, .14805)
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3774. 3801
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gene="At2q36830"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Jeres: 97088
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                                                   repeat_region
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gene

mRNA

CDS

gene

mRNA

CDS

us-09-938-842a-1034.oli.rge

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complement(40567. .42581)

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repeat\_region repeat\_region Arabidopsis thaliana Atlg58100 gene, complete cds. BT008493 TF08493.1 GI:30725659

JOCUS DEFINITION ACCESSION JERSION KEYWORDS

RESULT 7 3T008493

ORGANISM

RFERENCE AUTHORS

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BQGGGGVFAAHTSPLLGFHHQLQHHQNQNQNQDPVET I PEGENFSRKRYRSVDLSKEN
DDRKQNENEXLEXSETSGPTAA ÞMMAYAPPSRSGAGNTFWML PVPTTAGNQMESSSNN
NTAAGHRAPPMPFVNSAGGAGGGGAATHFWAGTGFS FPMDQYRGSPLQLGSFLAQ
PQPTQNLGLGAPDSNLGMLAALINSAYSRGGNANANABQANNAVEHQEKQQQSDHDDDS
REENSNSSE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AY081344 1479 bp mRNA linear PLN 24-MAR-2002 Arabidopsis thallana auxin-induced basic helix-loop-helix transcription factor, putative (At1958100) mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Sparmatophyta, Sparmatophyta, Sparmatophyta, Sparmatophyta, core eudicots, rosids, eurosids II; Brassicales, Brassicaceae, Arabidopsis.

(bases 1 to 1479)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Salk, Stanford, PGEC (SSP) Consortium members carried out the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequencing and annotation of the RAFL cDNAs: Nguyen, M., Southwick, A., Karlin-Neumann, G., Lam, B., Miranda, M., Palm, C.J., Swetr, L., Jones, T., Bahh, J., Chen, H.; Cheuk, R., Chung, M.K., Kim, C., Lin, J., Liu, S.X., Pham, P.K., Sakano, H., Shinn, P., Yamada, K., Ecker, J., Theologis, A. and Davis, R.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA 94304,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nguyen, M., Karlin-Neumann, G., Southwick, A., Lam, B., Miranda, M. Palm, C.J., Bowser, L., Jones, T., Banh, J., Carninci, P., Chen, H., Chung, M. K., Hayashtzaki, Y., Ishida, J., Kamiya, A., Kawai, J., Kim, C., Lin, J., Liu, S. K., Narusaka, M., Pham, P. K., Sakano, H., Sakurai, T., Satou, M., Seki, M., Shinn, P., Yamada, K., Shinozaki, K., Bcker, J., Theologis, A. and Davis, R. W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (26-FEB-2002) DNA Sequencing and Technology Center Stanford University, 855 California Avenue, Falo Alto, CA:94:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2.1%; Score 23; DB 8; Length 1206;
100.0%; Pred. No. 6.2;
ive 0; Mismatches 0; Indels
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                               /note="This clone is in
ecotype: Columbia"
1. .1206
                                                                                                                                                                     'note="unknown protein"
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chromosome="1"
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Best Local Similarity 100.
Matches 23; Conservative
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE
JOURNAL
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KEYWORDS
SOURCE
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AY081344
                                                                                                                                   SCO
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

I (bases 1 to 1206)
S Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Carninci,P.,
Ramiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
Narusaka,M., Nguyen,M., Ondera,C.S., Palm,C.J., Quach,H.L.,
Sakurai,T., Satou,M., Seki,M., Southwick,A., Toriumi,M., Wong,C.,
Theologis,A. and Ecker,J.R.
Arabidopsis ORF clones
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Dale,J.M., Hayashizaki,Y., Hsuan,V.W., Ishida,J., Jones,T.,
Naruiya,A., Karlin-Neumann,G., Kawai,J., Lam,B., Lin,J., Miranda,M.,
Narusaka,M., Nguyen,M., Onodera,C.S., Pallm, C.J., Quach,H.L.,
Sakurai,T., Sabou,M., Sekt,M., Southwick,A., Toriumi,M., Wong,C.,
Wu,H.C., Yamada,K., Yu,G., Yuan,S., Shinozaki,K., Davis,R.W.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Direct Submission
Submitted (15-MAY-2003) Salk Institute Genomic Analysis Laboratory
(SIGNAL), Plant Biology Laboratory, The Salk Institute for
Biological Studies, 10010 N. Torrey Pines Road, La Jolla, CA 92037,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RIKEN Genomic Sciences Center (GSC) members carried out the collection and clustering of RAFL cDNAs (RAFL cDNA: 'RIKEN Arabidopsis Full-Length cDNA'): Seki,M., Narusaka,M., Ishida,J., Satou,M., Kamiya,A., Sakurai,T., Carninci,P., Kawai,J., Hayashizaki,Y. and Shinozaki,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The Salk, Stanford, PGEC (SSP) Consortium members constructed and sequenced the pUNI (ORF) clones using the RAFL cDNAs: Cheuk,R., Chen,H., Kim,C.J., Shinn,P., Bowser,L., Chan, M.M., Chang,C.M., Dale,J.M., Hsuan,V.W., Jones,T., Karlin-Neumann,G., Lam,B., Lee,J.M., Lin,J., Miranda,M., Nguyen,M., Onodera, C.S., Palm,C.J., Quach,H.L., Southwick,A., Tang,C.C., Toriumi,M., Wong,C., Wu,H.C., Pandad,K., Yu,G., Yuan,S., Davis,R.W., Theologis,A., and
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                            Query Match
2.3%; Score 25; DB 8; Length 134151;
Best Local Similarity 100.0%; Pred. No. 0.42;
Matches 25; Conservative 0; Mismatches 0; Indels 0;
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(bases 1 to 1206)

TITLE JOURNAL EFERENCE AUTHORS

TITLE JOURNAL

COMMENT

Cheuk, R. (SSP/Salk) and Seki, M. (RIKEN GSC) contributed equally to this work. Shinozaki, K. (RIKEN GSC) and Ecker, J.R. (SSP/Salk) contributed equally to this work as PIs. Location/Qualifiers

Source

EATURES

organism="Arabidopsis thaliana"

/mol\_type="mRNA"

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Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-08.mit.edu/GENSCAN.html), Genemark.biology.gatech.edu/dLML), Genemark.biology.gatech.edu/dLML), Genemark.Bordovsky, http://genemark.biology.gatech.edu/dLML), Genemark.Bordovsky, http://genemark.biology.gatech.edu/dLML], GilmmerA (a variant http://www.tigr.org/scfilab/glimmerA.htm/glimmerA.html, and GeneSplicer (Mihaela Pertea.and Steven Salzberg, contact mperteagetigr.org), searches of the complete sequence against a peptide database and the plant EST database.ar TIGR (http://www.tigr.org/tdb/tgl.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with shinlarity to other proteins are named after the database hits. Genes without significant peptide similarity-but with EST similarity are named as unknown proteins or EST similarity but with EST similarity are named as unknown proteins over most of their length are annotated as hypothetical proteins Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.washington.edu/mk/RepeatMasker.html).

Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/mk/RepeatMasker.html).
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EQGGGGVFAAHTSPLLGFHYQLQHHQNQNQNQDPVETIPEGENFSRKRYRSVDLSKEN
DDRKQNENKSLKESETSGPTAAPMWAVAPPSRSGAGNTFWMLPVPTTAGNQMESSSNN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="qI:12321379"
/translation="KLPLDLEESILPRVPPRSLVRPRSVCREWNTLFKNKRFINKNFA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CGRPEIMLNTHSHIYSISVDLKDENPTIKVRDLRFDHLSCRGYHLYGICDGNFPMYSF
LNGGGGVVWNPLFWRQTKWIAKAENTCGKAIGYDGSRPEKSYKIIGRSSCSWQGKVTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYSVFEFATNAWKVTDHTRFHEKPELMDDSGRVSLNGNLYWTAYNSPHTGQYFIAMLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FSKEIEKSRKTFCVLPCKGEKSTTHTRILSIYKGDRFSVLEQSKKTREIEIWVTKDQI
GNGDDGDDVVMIKFWTVSRPDFPLLLSYISTSYFVDNDIHGKSFVLCCPSKRPKAAWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="similar to auxin induced basic helix-loop helix transcription factor GI:5731257 from (Gossypium hirsutum)" complement (<2159, :>3364)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ntaaghrappmmppynsagggaggggaathpmagtgfspepmdoyrgsplolgsplad
Poptonlglsmpdsnlgmlaalnsaysrggnananaeqannavehqekqqqsdhddds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /tränslation="MDLSDIRNNNNPTAAVATGGGARQLVDASLSIVPRSTPPBDSTL
ATTSSTATATTTKRSTKDRHTKVDGRGRRIRMPALCAARVPQLTRBLGHKSDGBTIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to unknown protein GI:2262162 from (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana)" (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis thaliana) (Arabidopsis tha
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transcription factor, putative"
/protein_id="AaG50759.1"
/db.xref="G1:12321381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     product="hypothetical protein, 5' partial"
protein id="AAG50757.1"
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complement(2159. .3364)
/gene="T18124.2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Arabidopsis thaliana"
| mol type="genomic DNA"
| cultivar="Columbia"
| db xref="taxon:3702"
| chromosome="I"
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/rpt family="AT_rich"
complement(45947 .4638)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="T18I24.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="T18124.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="T18124.1"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            codon start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . .85961
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EQGGGGVFAAHTSPLLGFHHQLQHHQNQNQNQDPVETIPBGENFSRKRYRSVDLSKEN
DDRKQNENKSLKESETSGPTAAPMWAVAPPSRSGAGNTFWMLPVPTTAGNQMESSSNN
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/product="auxin-induced basic helix-loop-helix

transcription factor, putative"

/protein id="AAL91233.1"

/protein id="AAL91233.1"

/protein id="AAL91233.1"

/protein id="AIN918999"

/translation="MULSDIRWINDTAAVATGGGARQIVDASLSIVPRSTPPEDSTL

/translation="MULSDIRWINDTAAVATGGGARQIVDASLSIVPRSTPEDSTL"
ATISSTATATITERSIKDRHTKVDGRGRRIRMPALCAARVPQLTRELGHKSDGETIEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NTAAGHRAPPMWPFVNSAGGGAGGGGAATHFMAGTGFSFPMDQYRGSPLQLGSFLAQ
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Arabidopsis thaliana chromosome 1 BAC T18124 genomic sequence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (pases 1 to 85961)
Lin.X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thaliana chromosome 1 BAC T18124 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ?OPTONLGLSMPDSNLGMLAALNSAYSRGGNANANAEQANNAVEHQEKQQQSDHDDDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-7aN-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Jan 19, 2001 this sequence version replaced gi:12280859. Address all correspondence to:at@tigr.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          BAC clone T18124 is from Arabidopsis thaliana chromosome 1
The orientation of the sequence is from SP6 to T7 end of the BAC
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Town,C.D. and Kaul,S.
Direct Submission
Submitted (19-AUG-2000) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org
3 (bases I to 85961)
Town,C.D. and Kaul,S.
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2.1%; Score 23; DB 8; Length 1479;
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Matches 23; Conservative 0; Mismatches 0; Indels
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/note="This clone is in pBluescript
ecotype: Columbia"
                                                                                     organism="Arabidopsis thaliana"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                note="synonym: T15M6.11"
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                       Ltype="mRNA"
xref="taxon:3702"
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        Location/Qualifiers
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| gene="At1g58100"
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                                                                                                                                                                                                         chromosome="1
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AC079131
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SOURCE
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AUTHORS
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AUTHORS
TITLE
JOURNAL
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FEATURES
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YLDVAÑATNI SLTLONDFSYRNTVLSTORGVOELDRNKNAODAAFYSGASFIKKKSRO
RDSLVATGACPSWLPFARENGGGKNLGALYMSQDATVI SSERKNYAEPPSHDPKMLSS
EENNSNPSPVTYEADNTKRAKQQFAQRSRVRKLQYI SELERNVOTLQAEGSKVSAELD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLNQRNLILSMENKALKKRLESIAQEKLIKQYSTVLKIVYLMSSVYYPVBQEVLEKBI
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activator (join(<5299. 537,512 from (Nicotiana tabacum)"
complement (join(<5299. 5357,5415. 5651,5738. 5864,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GSRHGQKLSNEKTHHQRTSSESHLVEELPFWLDDLLNEQPESPARKCGHRRSS
                                                                                                                                                                                                                                                                                                                 complement(join(5299, .5357,5415, .5651,5738, .5864,
5968, .6043,6135, .6853))
/gene="T18124.3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "note="predicted by genemark hmm"
oin(<10149. .10243,10536. .>11703)
gene="T18124.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .....tu149. .10243,10536. .11703)
gene="T18124,4"
codon ---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (8504. .8535)
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complement (8599. .8627)
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10149. .11703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement (10335. .10360)
2 15:24:10 2004
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                                                                                                                                                                                                          QXQSLVATGRKILGITEEDÄREKALRKLEDVILEPPRÄASRKSRTYFKRTRYLPDIMG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /trānslation="MASNNVPFQVPVLTKSNYDNWSLRWKAILGAHDVWBIVEKGFIE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polyprotein GI:6850900 from
                                                                                                                                                                                                                                                                                                                                                 /rpr family="(GAGAA)n"

complement (12815. 13163)

gene="T18124.17"

/note="Beeudogene, putative heat shock transcription
factor HSP30"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -"copia-type polyprotein, putative"
-id="AAG50765.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note="similar to copia type
(Arabidopsis thaliana)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            t family="AT rich"
5]ement (1490]. .18863)
6="T18124.5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Complement (13870. .13965)
/rpt family="AT rich"
complement (14034. .14074)
/rpt family="AT rich"
complement (14182. .14205)
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gene

mRNA

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VLRSLDLKPEHIVTVIEETKDLEAMTIBQLLGSLQAYBEKKKKKEDIVEQVLNMOITK BENGQSYQRRGGGQVRGRGRGGYGNGRGWRPHEDNTNQRGENSSRGRGKGHPKSRYDK SSVKCYNCGKFGHYASECKAPSNKKFEEKANYVEEKIQEEDMLLMASYKKDEQEENHK VDPTTFKSLVGSLRYLTCTRPD1LYANGVVSRYMEHDTTTHFKAAKRILRY1KGTVNF GLHYSTTSDYKLVGYSDSDWGGDVDDRKSTSGFVFY1GDTAFTWMSKKQP1VTLSTCE LMSYYLGIEVKQEDNGIPITQEGYAKEVLKKFKMDDSNPVCTPMECGIKLSKKEEGEG AEYVAATSCVCHAIWLRNLLKELSLPQEBPTKIFYDNKSAIALAKNPYFHDRSKHIDT RYHYIRECVSKKOVQLEYVKTHDQVADIFTKPLKREDFIKMRSLLGVAKSSLRGGVES

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h 2:1%; Score 23; DB 8; Length 85961; Similarity 100:0%; Pred. No. 4.4;
                         0; Indels
                           0; Mismatches
                                                                   3190 TCGACTAAAGACCGTCACGAA 3168
                                                        220 TCGACTAAAGACCGTCACACGAA 242
                           23; Conservative
Query Match
Best Local S
                            Matches
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Enkaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnollophyta, eudicotyledons, core eudicots; rosids; eurosids II. Brassicales, Brassicaceae, Arabidopsis.

1 (bases I to 103637)

Lin,X., Kaul,S., Town,C.D., Benito, M. I., Creasy, T. H., Haas,B.J., Wu,D., Maiti,R., Roming,C.M., Koo,H., Fujii,C.Y., Utterback,T.R., Arabidopsis thallana chromosome 1 BAC T15M6 genomic sequence
                                               T15M6 genomic sequence,
                                             AC079604 103637 bp DNA Arabidopsis thaliana chromosome 1 BAC
                                                                                                                                                                Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
                                                                                                                           AC079604.5 GI:12321249
                                                                                  complete sequence.
                                                                                                                                                                                                                                                                                                                                                                              Unpublished
RESULT 10
AC079604/c
LOCUS
DEFINITION
                                                                                                 ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
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JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
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AUTHORS
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Submitted (04-SEP-2000) The Institute for Genomic Research, 9712. Medical Center Dr. Rockville, ND 20850, USA, cdrown@tigr.org 3 (bases 1 to 103627)
Town,C.D. and Kaul,S. Submitted (19-JAN-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdrownerigr.org On Jan 19, 2001 this sequence version replaced gi:12280852. Address all correspondence to:at@tigr.org (bases 1 to 103637)
own, C.D. and Kaul, S.
irect Submission Direct Submission REFERENCE AUTHORS TITLE JOURNAL COMMENT

prediction programs including Genscan+ (chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GenemarkHMM (Mark Borodovsky http://genemark.biology.gatech.edu/Genemark/), GlimmerA (a variant of GlimmerM, see Mihaela Pertea, BAC clone TISM6 is from Arabidopsis thallana chromosome 1 The orientation of the sequence is from SP6 to T7 end of the BAC Genes were identified by a combination of several methods. Gene of GlimmerM, see Mihaela Pertea, http://www.tigr.org/softlab/glimmerm\_htm/glimmerm.html, and clone.

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repeat_region
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                                                                                                                                      CDS
mperteagligr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Amnotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE). Simple repeats are identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TA FAAI INREKETRWI ILSIIGSILIYVEGSPEFGGEPDENBEFYSIQAWLTFÄASV
AFALSLCEPQLCFEKYLVKTRYGYKSYFRWT IRMQICVSFATVOTUGTBAGBUK
AFQCDSHEKKGEFYYVLSLI GALSWQVRANGLMGIYLYVGSVFGDVVHMCTSPLVA
LFVVLAFDFMDDEFSWPRIGTLIATVVALGSYFYTLHKRNKKKMVELYQTENNIDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPKQNQETTNTRFLSFRLILLYISLGVLVAAHSKLFALGKLYANFGVFTLISATQLIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'tränglation="memteaskottaegsanpepdoilsprrsleikokkwmisvsilc
|FIVLIGDSIVMLLINFFYVQDNREDSDQDLQYRGTMLQALVQNAAFPLLIPLFFIFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="pseudogene, putative non-LTR retroelement reverse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            note="pseudogene, hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (8659. . 8680)
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complement (10552. . 10573)
/rpt_family="AT_rich"
complement (10742. .10991)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           'product="unknown protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement (3359, .4729)
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complement (<3359. .>4729)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /rpt_family="AT_rich"
complement(12070..17708)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /rpt_family="AT_rich"
complement(6713. :6740)
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complement(7047. 7147)
/rpt_family="AT_rich"
complement(8659. :8680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement (18837. .23614)
/gene="T15M6.22"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement (11760. .11838)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (1003. ,1088)
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complement (1091. ,2595)
/gene="T15M6.25"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement (3557. .4729)
gene="T15M6.24"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(1. .663)
/gene="T15M6.26"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          gene="T15M6.4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 gene="T15M6.23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone="T15M6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /map="?"
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SLIVIKKIMKMEAADPRNVPVNPEALGIPDYFDIIKTPMDFGTICNNFEKGNKYMNSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DKTOSI DRSMBETGDEPVNSAAEKLIVVIAŠIEGPKSTONEEEEKEKRLOBOKKRIJELE
RKEWRMKMORKFOVRNPOLLSLCETLFPNDNNHNSVWNGPHSLFRRGGSNRSSALHK
AVESLANBLANSLSYALGARSLFAMLDESGYPHTLRAATSNASI FIISTKAIGEYASL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DVYKDVNYIWNNCSKYNKKGDYIVDIMKRVKKNPMKYWTSAGIYTEOSAAENTEDGGK
ASTKQKSHKRHGRHHKSDCMCAICVIKRRKERERDSGAQEESSPAGSPSVDNSSVNM
GEDWDIDVDKKPEQEKITEIVELDSPVSKTYRNIENKQEVEEEENVEVESENKTKANVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISKAVELTLITDWRLLLINKCWKSBAKRRCDDABAYAGGERSRIDPYPODWWGSELLR
AAVSIPVSPRITKPTEEGROSRSQSLLGVGWELWSPVAEIIRRSSEPSGCLVQSGDGA
ROQGWCGEIVLAMHCLCEVLLIRAPLCYL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="pseudogene, putative retroelement pol polyprotein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="contains similarity to maleless protein (mle) (21:57905 from (brosophila melanogaster)" complement (join(<40407 .40527,40617.14039,40922. 41217 .41405,41490 .41576,41787 .41853,41997 .4244405 .41405,41490 .42597,42686 .42769,42978 ..43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note="pseudogene, putative cationic amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6206. .46328,46511. .46587,46694.
7463. .47681,47870. .48243,48329.
8927. .49132,49211. .49316,49403.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (30166. .30215)
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complement (32488. .32485)
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complement (32589. .33008)
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complement(39499".39523)
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39684.39687.
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complement(40447.39696)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /rpt_family="(A)n"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement (39320. .39376)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /rpt_family="AT_rich"
complement(33893. .33928)
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37880. .38594
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene="T15M6.6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'gene="T15M6,20"
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1.8%

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'translation="MAPTKKPQKNKQSKNEIASSLIPNSGHKKPSKAPKLISPENED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dermatophagoides farinae (American house dust mite)

Dermatophagoides farinae

Bukaryota; Metazoa, Arthropoda; Chelicerata; Arachnida; Acari;

Acariformes; Sarcoptiformes; Astigmata; Psoroptidia; Analgoidea;

1 (Lases I to 2134)

1 (Lases I to 2134)

Tsai L. C., Chao, P. L., Shen, H. D., Tang, R. B., Chang, T. C., Chang, P. L., Shen, H. D., Tang, M. W., Lee, B. L., and Chua, K. Y.

Isolation and characterization of a novel 98-kd Dermatophagoides
                                                                                                                                                                                                                                                                                                                                                                                                             ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AF352244 2134 bp mRNA linear INV 25-APR-2001
Dermatophagoides farinae paramyosin-like allergen mRNA, partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="paramyosin-like allergen"
/protein id="AAK39511.1"
db_xref="G1:13785807" "A"
/translation="WHKRDSBLAKLRKLLEDVHIESEETAHHLROKHQAAIQEMQDQ
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42272. 42409,42496. 42597,42686. 42769,42978. 43034,
43117. 43206,43297. 43437,43824. 43928,44669. 44221,
44305. 4448944502. 44607,44691. 448474,44972. 45057,
45292. 45357,45493. 45550,45745. 45845,46042. 4519,
46206. 46328,46511. 46587,46694. 46882,46982. 47093,
47463. 47681,47870. 48243,48329. 48479,48788. 48823,
48927. 49115M6.6"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 2134)
Tsai,L., Sun,Y., Chao,P., Ng,H., Hung,M., Hsieh,K., Liaw,S. and
Chua,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Teai,L.-C., Chao,P.-L., Ng,H.-P. and Chua,K.-Y.
Teai,L.-C., Chao,P.-L., Ng,H.-P. and Chua,K.-Y.
Direct Submission
Submitted (22-FEB-2001) Medical Research, Veterans General
HOSpital-Talpei, No. 201, Sec. 2, Shih-Pai Road, Taipei, Taiwan
112, Republic of China
                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                           Score 23; DB 8; Length 103637; Pred. No. 4.3;
                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
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8389068
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             llergen in Dermatophagoides farinae
lin. Exp. Allergy 29 (12), 1606-1613 (1999)
0062524
                                                                                                                                                                                                                                              product="hypothetical protein"
protein_id="AAG50700.1"
db_xref="G1:12321256"
                                                                                                                                                                                                                                                                                                                                             2.1%; Scot.
100.0%; Pred. No. ...
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75568 TCGACTAAAGACCGTCACAAA 75546
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/db_xref="taxon:6954"
/clone="Derf11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                220 TCGACTAAAGACCGTCACACGAA 242
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                                                                                                                                                                                                                           codon_start=1
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/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                      23; Conservative
                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0594536
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AF352244
LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACCESSION
FERSION
(EYWORDS
)OURCE
ORGANISM
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MEDLINE
PUBMED
(EFERENCE
AUTHORS
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AUTHORS
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CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUBMED
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ERKRASIENHAHTLEVELESIKVOLDESERARLELEROLTKANGDASAWKSKYEAELD
AVDEVERELERRONGKYESPEQLEALINKCSSIERKKSKTANGDASAWKSKYEAELD
AVDLEKKVAOLIEKINDLKAKLEESTKKKSTALOSEUGHTINDLEKATRI
AQOLEKKVAOLIEKINDLKAKLEESTWILMEOSAKLISEKKKSTALOSEUCHEYSEKLROORD
GLARENKKLTDDLAARKSQLNDAHRRIHEGEIEIKRIBBRDELSAYKEAETLEKOGE
ARKORULIAELAQVRHYYERRIAGODEEIBLIKKOYOI EIGUNMILAEABAKLKYEI
ARLKKKYOAOLITELELELDAANKANIDLOKTIKKOALOITELOAHYDEVHROLOGAYO
GLGYTORROCALOAELEEMRIALEOANRAKROAEQLHEEAVKYNELTINNALASAK
ISQENSTILHYRIESUSANMALAGGKKVIAKLIEKSTKDLIIESCHRUKLIAASAK
DHRVKELLIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ostropicuscinae; vapic.

Akhter, N., Antonellis, A., Ayele, K.; Becketrom-Sternberg, S.M., Benter, N., Antonellis, A., Bouffard, G.G., Breen, K., Brinkley, C., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Haghighi, P., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, B., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Mankeri, B., Margulies, B. H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Paguirigan, C., Pearson, R., Portroy, M.B., Praenada, A., Schuelerjm, G., Stantripop, S., Thomas, J. W., Touchman, J.W., Teurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, B.D. NISC, Comparative Sequencing Initiative
BINRTVIELTSHKORLSQENTELIKEVHEVKLOLDNANHLKTQIAQQLEDTRHRLEEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC124912 149452 bp DNA place linear HTG 16-JUL-2002 Papio anubis clone RP41-205M12, WORKING DRAFT SEQUENCE, 4 ordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC124912.2 GI:21844567
HIG; HTGS PRAFT.
Papio anubis (olive babon)
Papio anubis
Papio anubis
Relative (olive babon)
Papio anubis
Papio anubis
Papio anubis
Papio anubis
Papio anubis
Craniata, Vertebrata, Euteleostomi;
Mammalia, Butheria, Prinates, Catarrhini, Cercopithecidae;
Cercopithecinae; Papio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (19-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD 20877, 198A 5
3 (bases 1 to 149452)
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On Jul 16, 2002 this sequence version replaced g1:21455384.
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                                                                                                                                                                                                                                                                                                                                                                                              Score 22; DB 3; Length 2134; Pred. No. 19; 200
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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100.0%; Pre
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                                                                                                                                                                                                                                                                                                                354 C
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Best Local Similarity 100.
Matches 22; Conservative
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DRAFT.

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Akhter, N. Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B., Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S., Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P., Hansen, N. Ho, S.-L., Idol, J.R., Karlins, E., Laric, P., Lee-Lin, S.-Q., Legaspi, R., Waduro, Q.L., Madtro, V.B., Margulies, E.H., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C., McDowell, J., Pagnirigan, C., Pearson, R., Portnoy, M.C., Parad, A., Schueler, M.G., Stantripop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L., Young, A., Zhang, L.-H. and Green, E.D., NISC. Comparative Sequencing Initiative
Papio anubis clone RP41-382N23, WORKING DRAFT SEQUENCE, 4 ordered
                                                                                                                                                                                                         Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Buteleostomi, Mammalia; Butheria; Primates; Catarrhini; Cercopithecidae; Cercopithecinae; Paplo:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (28-JUN-2002) NIH Intramural Sequencing Center, 8717
Grovemont Circle, Gaithersburg, MD/20877, USA 8
3 (bases 1 to 170737)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (20-JUL-2002) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA On Jul 20, 2002 this sequence version replaced gi:21622721.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Center: NIH Intramural Sequencing Center
                                                                                                                                                Papio anubis (olive baboon)
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DEFINITION
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have provided by the submittor.

* This sequence will be replaced
* by the finished sequence as soon as it is available and the accession number will be preserved.

* 1874% 1874; contig of 1874 bp in length
* 1874% contig of 18637 bp in length
* 1274% 1274% contig of 19833 bp in length
* 14717; gap of unknown length
* 14718 14717; gap of unknown length
* 14758 147017; contig of 1933 bp in length
* 14718 14717; gap of unknown length
* 14718 14717; gap of unknown length
* 14718 14717; gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8x average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                           Insert size: 150000; agarose-fp
Insert size: 149152; sum-of-contigs
Quality coverage: 11.35x in Q20 bases; agarose-fp
Quality coverage: 11.42x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                  Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319 consensus quality: 148556 bases at least Q30 consensus quality: 148773 bases at least Q30 consensus quality: 148773 bases at least Q20
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note="assembly_fragment"
27585. .147017
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note="assembly_fragment
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18848. _.127484
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Genome Center

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The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contigl has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR resting. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequencing vector: plasmid; n/a; 100% of reads Chemistry: Dye-terminator Big Dye; 100% of reads Assembly program: Phrap; version 0.990319
Consensus quality: 120910 bases at least Q40
Consensus quality: 170146 bases at least Q30
Consensus quality: 170296 bases at least Q20
Insert size: 162000; agarose.fp
Quality coverage: 11.73x in Q20 bases; agarose.fp
Quality coverage: 11.73x in Q20 bases; sum-of-contigs
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Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@nhgri.nih.gov
Contact: project Information
Center project name: cyt
Center clone name: 382N23
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HTG 20-JUL-2002

DNA

170737 bp

AC125510

RESULT 13 AC125510 LOCUS

Ouery Match 2.1%; Score 22; DB 2; Length 149452; Best Local Similarity 100.0%; Pred. No. 13; Matches 22; Conservative 0; Mismatches 0; Indels 0.

35684 TGGGTGAAATCTGATGAAGAA 35705

엄 ò

473 TGGGTGAAATCTGATGAAGAA 494

us-09-938-842a-1034.oli.rge

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ACO51640 158514 bp DNA linear HTG 24-AUG-2002
Homo sapiens chromosome 9 clone RP11-161B4 map 9, WORKING DRAFT
SEQUENCE, 25 unordered pieces.
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Birren, B., Linton, L., Nusbaum, C. and Lander, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Note="clone overlaps with GenBank Accession Number AC124912 clone RP41-205M12 (center project name cyu)" 46239, .164110 chote="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1...38014

/note="clone overlaps with GenBank Accession Number AC12511 clone RP41-427L1 (center project name cys)" /note="assembly_fragment" | 132730...146138
as soon as it is available and
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          the accession number will be preserved.

1 89919: contig of 89919 bp in length

8 9020 90019: gap of unknown length

146139 146238: gap of unknown length

146239 146238: gap of unknown length

146239 16410: contig of 17872 bp in length

164211 164210: gap of unknown length

164211 170737: contig of 6527 bp in length

164211 170737: contig of 6527 bp in length.
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35046 c 32826 g 47413 t
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/db_xref="taxon:9555"
/clone="RP41-382N2"
/clone="RP41"
                                                                                                                                                                                                                                                                                                                                                                                                                       /note="assembly_fragment
clone_end:SP6
vector_side:left"
                                                                                                                                                                                                                                                                      organism="Papio anubis"
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AC051640.4 GI:9966320
HTG: PHGS PHASEI; HTGS DRAFT.
Homo sapiens (human)
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AUTHORS
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AL SUBmitted (15-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA 3 (bases 1 to 158314).

Shirren, B., Linton, L., Nusbaum, C., Lander, B., Abraham, H., Allen, N., Boukhgalter, B., Brown, A., Burket, G., Campoplano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Costle, P., Fitzhugh, W., Gage, D., Callins, S., Collymore, A., Goyette, M., Grand-Pierre, N., Diaz, J.S., Dodge, S., Ferreira, P., Fitzhugh, W., Gage, D., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, N., Landerst, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Macdonald, P., Marquis, N., McCarthy, M., McEwan, P., McKernan, K., McCarthy, T., Naylor, J., Ninoya, T., Managa, V., McCarthy, T., Naylor, J., Ninoya, T., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Santos, R., Schauer, S., Severy, P., Strauss, N., Subramanian, A., Stange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Nilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson, B., Wilson,
Levine, R. Lieu, C., Liu, G., Locke, K., Landers, T., Lehoczky, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marquis, N., McGarthy, M., McBwan, P., McGurk, A., McRernan, K., McPheeters, R., Meldrim, J., Menos, L., Mihow, T., Miranda, C., Mlenga, V., Morrow, J., O'Rail, D., O'Lyar, T., Moliver, J., Peterson, K., Pierre, N., O'Nail, D., O'Divar, T.M., Oliver, J., Peterson, K., Pierre, N., Pisani, C., Pollara, V., Raymond, C., Riley, K., Rogov, P., Rothman, D., Stange-Thomann, N., Schauer, S., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Tirrell, A., Travers, M., Trigilio, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G., Zainoun, J., Zimmer, A. and Zody, M., Kyman, D., Ye, W.J., Direct, Submission
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Center: Whitehead Institute/ MIT Center for Genome Research
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Center clone name: 161 B 4

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Sequencing vector: M3: M7815; 93% of reads
Sequencing vector: Plasmid; n/a; %-0.f%% of reads
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Consensus quality: 136255 bases at least Q40
Consensus quality: 147839 bases at least Q30
Consensus quality: 152536 bases at least Q20
Insert size: 159000; agarose-fp
Insert size: 16114; sum-of-contigs
Quality covverage: 3.4 in Q20 bases; agarose-fp
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Human DNA sequence from clone RP11-23B15 on chromosome 9, complete
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This sequence was finished as follows unless otherwise noted: all
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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On or before May 15, 2001 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2.0%; Score 21; DB 2; Length 158514; 100.0%; Pred. No. 41;
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abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; T:, TREMBL; WORMPEP; Information on the WORMPEP, database can be found at http://www.sanger.ac.uk/Projects/Celegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 9, constructed by the Sanger Centre Chromosome 9 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr9 RPII-23B15 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see http://www.chori.org/bacpac/home.htm
                                                                                                                                                                                                                                                                                                            This sequence is the entire insert of clone RP11-23B15 The true right end of clone RP11-54606 is at 35092 in this sequence. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIMC5 repeat: matches 7595. .7936 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                76. .3130
ote="LIMC5 repeat: matches 6976. ,7233 of consensus!
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .7595 of consensus'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ote="L1PB3 repeat: matches 5964. .6141 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          repeat: matches 2293. .2709 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . .2870
.e="MLTIG repeat: matches 14. .536 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66. .6870
| ote="MER86 repeat: matches 25. .132 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                186. .8450
Hote="MER47A repeat: matches 2. .366 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    .2419 of consensus"
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hote="MLT2FA repeat: matches 1. .400 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="SVA repeat: matches 552. .1259 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .1828 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat: matches 14. .131 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .uSx repeat: matches 1. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          160. .12130
| Ote="L2 repeat: matches 200. .2168 of consensus"
| 131. .12507
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeat: matches 1. .371 of consensus"
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te="AluSx repeat: matches 2. .310 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ote="MER81 repeat: matches 1. .107 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="MER20 repeat: matches 1, .214 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     te="AluJo repeat: matches 1. .286 of consensus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat: matches 79. .130 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              te="L1MC5 repeat: matches 7282.
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mol_type="genomic DNA"
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89. .503
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note="Charlie4 repeat: matches 1795. .1952 of consensus"
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....21126
="LiMB2 repeat: matches 5953. .6164 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="AluSp/q repeat: matches 212. .297 of consensus"
                                                                         note="L1M4 repeat: matches 3221. .3374 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                note="L1MB8 repeat: matches 5875. .6168 of consensus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                repeat: matches 5433. .5742 of consensus"
                                                                                                               note="AluSx repeat: matches 1. .288 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Til repeat: matches 19. .137 of consensus"
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                                                                                                                                                                                                                                                                                                                  ote="AluSq repeat: matches 1. .313 of consensus"
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                                                                                                                                                          repeat: matches 18. .184 of consensus"
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                                        .954 of consensus"
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note="Alusq repeat: matches 1. .313 of consensus"
1600. .29946
100te="Limbs repeat: matches 5817. .6171 of consensus"
                                                                                                                                                                              708. .31108
.ote="L1MB4_repeat: matches 5781. .6183 of consensus"
                                                                                                                                                                                                                                                                                                                                                                                                      ote="LIMB4 repeat: matches 5081. .5786 of consensus"
                                                                                                                                     953. .30009

0cte="L2 repeat: matches 2671. .2729 of consensus"

708. .31108
note="L2 repeat: matches 2407. .2668 of consensus"
                                    100te="MIR repeat: matches 100. .262 of consensus"
9269. .29580
                                                                                                                                                                                                                                                                                                                                                                                                                 2005. .32312
note="AluJb repeat: matches 1, .308 of consensus"
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lote="29 copies 2 mer at 75% conserved"
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Query Match Best Local Similarity 100.0%; Pred. No. 41; Matches 21; Conservative 0; Mismatches 0; Indels 0

12691 GTTGAAGGAAGAGGAAAGG 12711 244 GITGAAGGAAGAGGAGAAGG 264  $\delta$ g

Search completed: February 2, 2004, 07:55:25 Job time : 4077.3 secs

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GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  M nucleic - nucleic search, using sw model  *Un on: February 1, 2004, 21:59:06; Search time 313.739 Seconds  (without alignments) 9214.976 Million cell updates/sec  fitle: US-09-938-842A-1034 9214.976 Million cell updates/sec  originates: 1071 Searched: 0.1070 Searched: 0.1070 Searched: 2552756 seqs, 1349719017 residues  *Ord size: 0  Cotal number of hits satisfying chosen parameters: \$105512  finimum DB seq length: 0 faximum DB seq length: 20000000000  ost-processing: Listing first 45 summaries	N Geneseq 19Jun03:*   S1DS1/gcgdata/geneseqn-emb1/NA1980.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1981.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1982.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1982.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1983.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1985.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1985.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1986.DAT:*   S1DS1/gcgdata/geneseqg-ensegqn-emb1/NA1989.DAT:*   S1DS1/gcgdata/geneseqg/geneseqqn-emb1/NA1989.DAT:*   S1DS1/gcgdata/geneseqg/geneseqqn-emb1/NA1999.DAT:*   S1DS1/gcgdata/geneseqg/geneseqqn-emb1/NA1999.DAT:*   S1DS1/gcgdata/geneseqg/geneseqqn-emb1/NA1991.DAT:*   S1DS1/gcgdata/geneseqg/geneseqqn-emb1/NA1992.DAT:*   S1DS1/gcgdata/geneseqf/geneseqqn-emb1/NA1992.DAT:*   S1DS1/gcgdata/geneseqf/geneseqqn-emb1/NA1993.DAT:*   S1DS1/gcgdata/geneseqf/geneseqqn-emb1/NA1993.DAT:*   S1DS1/gcgdata/geneseqf/geneseqqn-emb1/NA1995.DAT:*   S1DS1/gcgdata/geneseqf/geneseqqn-emb1/NA1995.DAT:*   S1DS1/gcgdata/geneseqf/geneseqn-emb1/NA1995.DAT:*   S1DS1/gcgdata/geneseqf/geneseqf/geneseqn-emb1/NA1997.DAT:*   S1DS1/gcgdata/geneseqf/geneseqf/geneseqf/geneseqf/geneseqf/geneseqf/geneseqf/geneseqf/geneseqf/g	/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/genesed/genesed/ SIDS1/gcgdata/genesed/genesed/genesed/genesed/ SIDS1/gcgdata/genesed

Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.

Claim 144; SEQ ID NO 1034; 577pp + Sequence Listing; English.

The invention relates to identifying a stress condition to which a plant cell has been exposed, comprising a stress condition to which a plant cell has been exposed, comprising in the plant cell with an array or probes representative of the plant cell genome; and plant cell with an array or probes representative of the plant cell genome; and notice as stress response. The method is useful in the production of transgenic plants, cells and seeds and in producing plants broduction of transgenic plants, cells and seeds and in producing plants with increased tolerance to abiotic stress. The present sequence is that on a Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used not a Arabidopsis thaliana stress regulated gene (ABZ12196-ABZ17574) used specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 1071 BP; 287 A; 288 C; 256 G; 240 T; Oother;
Ouery Match

Ouery Match

Duery Match

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Ouery Matches 1071; DB 24; Length 1071;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps 0

120 301 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAGG 360 AATCTGATGAAGAAGAAACGTAAAACGACCTTCTAACAGTGAGTATATAGACATAAGGGGAC 540 09 GATCTAACCATCATCAACGCGTCAGAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT 120 cccacagradrercaagcccaaggcggagccggrgargccgrcgrrrrcaargrerrra 180 AAGGTTGAAGGAAGAAGAAGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTT 300 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG 360 361 AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGGCCATCGCCATG 420 TCGGTTAACGGAACCTTAAAAATCCCGACGACGACGAACGCTGATTCTGATATGGGTGAA 480 TCGGTTAACGGAACCTTAAAATCCCGACGACGACGAACGCTGATTCTGATATGGGTGAAA480 ATCTGATGAAGAAAAAAGTAAAAGGACCTTCTAACAGTGAGTATATAGACATAAGAGAGC 540 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACAACGATCCAAACGCTCCG 600 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGATCCAACGACGG600 TGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTCTTCAACCAAA720 09 CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 660 GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGCTTCGACTAAAAGACCGTCACACG GCTCCACCGTCTTCGACAGGACCACCATTGAAGAGAGCTTCGACTAAAGACCGTCACAC GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAACTTCAAGACCTTTCCAAGTAAAT CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA 241 AAGGTTGAAGGAAGAAGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTTTT ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 1 Arddcdacharirchdaadcrigaadarichdcadcchardarchardadccccri 61 181 241 421 481 541 601 601 61 121 121 181 301 421 481 541 199

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Novel Arabidopsis thalians nucleic acid useful for constructing

900 840 GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGGTAACAAACGGTTGATCGTCATCGTCA 721 ATCGCTGGTCCGTCGAATCAGCCTCAGTTATAGCTTTTCCCGCCGCCGCCGCTGCTTCGCCG 780 TGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACAA 720 781 TCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACAA GITGITCCAAGCAGCGGCTITGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAGA 841 GTTGTTCCAAGCAGCGTTTGTATCCGTTTCAGACGTTAGCGGTTCGAAGTTTATCAAGA GCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTCATCGTCA Haas WD; 1071 Thale cress; gene, ds; genetic manipulation; plant; blosynthesis; genetic modification; environmental stress; disease resistance; fungicide; insecticide; stress tolerance. TOGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCT Gorlach J, An Y, Hamilton CM, Price JL, Hargiss TR, Yu Y; Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, H Garcia CA; 1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA Arabidopsis thaliana polynucleotide #502 standard; DNA; 460 13-AUG-1999; 99US-148784P. 07-AUG-2001; 2001US-0924035 MATHEW A V. LEDFORD B L. WOESSNER J P. PRICE J.L. HARGISS T.R. Arabidopsis thaliana HAMILION C M. RAMBAKA J G. WPI; 2003-102509/09 US2002142319-A1 26-FEB-2003 781 196 1021 841 901 901 961 ABX61156 ABX61156 (WOES/) (HAAS/) (GARC/) RAME/) 성 읍 8 ð a ठ 용 ठ g ୪

genetic modification; gene, ss.

The invention relates to Arabidopsis thaliana nucleic acid sequences. The DNA sequences and the polypeptides they encode are useful for identifying homologous or related genes, for producing compositions that modulate the temperature of the polypeptides, for mapping functional capturesion or function of the polypeptides, for studying associated to physiological pathways, for genetic manipulation of cells, preferably plant cells, in screening assays of various plant strains that are capable of withstanding a particular disease or the strains that are capable of withstanding a particular disease or environmental stress, for enhancing or inhibiting production of cisynthetic products in plants and the sease resistance and stress are useful for introducing or improving disease resistance and stress collisions. Screening biologically active agents, such as plant cells and plants. Such as plant cells and plants is screening biologically active agents, such as functional agents, such as biosynthetic pathways of nutritional, commercial or medicinal value. Sequences ARSKOSSS-ARXASSS Tepresent Arabidopsis thaliana transgenic plant with enhanced disease resistance and enhanced traits of interest, as probes, and in diagnosis and screening purposes Claim 1; Page 158; 277pp; English.

Sequence 460 BP; 113 A; 103 C; 134 G; 109 T; 1 other;

polynucleotides of the invention,

1019 600 GCAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 659 719 GTGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACA 341 AATCGCTGGTCCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCNG-TTCGCC 282 222 GCAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGAT 401 AATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTCGCC 779 GTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTTTACA 839 AGTIGITCCAAGCAGCGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAG 899 959 AGTIGITCCAAGCAGCGCTTTGTATCCGTTTCAGACGTTAGCGGTTCGAATTTATCAAG 162 AGCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACGGTAGTTCATCGTC 102 42 GTGGGCTATTCCATCAAACGCAATGATTCCGACGGTCGGAGCTTTCTTCTTGATTCCACA Gredretracerececeretreacadecriceaceareceradaceacerecerraca AGCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACGGGTAGTTCATCGTC 960 AATTGCAACAACAACGACGCACACGCTGAGAGACTTCTCCCTAGAGATATACGAGAAACA Gaps 1, 27.0%; Score 289; DB 25; Length 460; 99.6%; Pred. No. 1.4e-131; 1; Indels 1020 AGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1060 41 AGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 0; Mismatches Conservative Query Match Best Local Similarity Matches 459; Conserval 340 281 900 460 099 00 720 280 840 221 161

ABL93850 standard; cDNA; 453 BP ESULT 3 BL93850/c

ABL93850;

(first entry) 10-JUN-2002

Arabidopsis thaliana nucleic acid sequence Ref:2027615 SEQ ID NO:615.

Arabidopsis thaliana; insecticide; fungicide; plant; mapping; diagnosis;

Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y, Rameaka JG, Page A, Mathew AV, Ledford BL, Moessner JP, Haas WD; Garcia CA, Kricker M, Slater T, Davis KR, Allen K, Hoffman N; Hurban P; 26-JAN-2001, 2001US-0770444. 27-JAN-2000; 2000US-178502P; HAMILTON C M. PRICE J L. Arabidopsis thaliana. LEDFORD B L. WOESSNER J P RAMBAKA J G. RAINES T M. MATHEW A V. GORLACH J. HOFFMAN N. HURBAN P. DAVIS K PALLEN K. US2002023280-A1. PAGE A 21-FEB-2002 (ALLE/) (HOFF/) (HURB/) (YUYY/) GORL/) ANYY/) HAMI/) (PAGE/) LEDF/) (WOES/) (HAAS/) (GARC/) 

WPI; 2002-267486/31.

New Arabidopsis thaliana nucleic acid, for identifying homologous genes, producing compositions that modulate the expression or function of its encoded protein, and mapping functional regions of a protein -

Claim 1; SEQ ID 615; 44pp; English.

The present invention describes an Arabidopsis thaliana nucleic acid (I) comprising a sequence capable of hybridising under stringent conditions to a sequence (Si) sealected from any one of the 399 sequences given in ABL93236 to ABL94234. (I) have insecticide and fungicide activities, and they can be used as protein expression modulators. (I) can be used in identifying homologous or related genes; in producing compositions that modulate the expression or function of their encoded proteins, mapping functional regions of the proteins, and in studying associated physiological pathways: (I) can also be used: (1) for the genetic manipulation of cells, particularly plant cells; (2) in screening assays of various plant strains to determine the strains that are best capable of various plant strains to determine the strains that are best capable of various plant strains to determine the strains that are best capable of various plant in disgenses or environmental stress; (3) for enhancing or inhibiting production of a biosynthetic product in a plant; (4) as probes in mapping and in diagnosis, in genetic modification and for some content of propersor of a biosynthetic production of consequence of the printed and (5) for generate ribozymes or as triple-stand forming oligonucleotides; and (5) for generating genetically modified transgenic organisms.

Whose: The sequence data for this patent, did not form part of the printed usper of the printed usper one steed the specification, but was obtained in electronic form at directly from the

ring series

Sequence 453 BP; 111 A; 100 C; 132 G; 107 T; 3 other;

Gaps .. 0 Query Match

26.7%; Score 286; DB 24; Length 453;
Best Local Similarity 100.0%; Pred. No. 4.3e-130;
Matches 286; Conservative 0; Mismatches 0; Indels

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TCGTCAATTGCAACAACAACGACGCACACGCTGAGAACTTCTCCCTAGAGATATACGAG 1014
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                                                                                                                                                                                             166 TCAAGAGCGACGTCGGTTATGGCTCCGAGCTCAAGCTCAGGCGTAACAACCGGTAGTTGA. 107
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                                                                                                                                                                    TCAAGAGCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACCGGTAGTTCA
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ABQ47102/c ID ABQ47102 standard; DNA; 755 BP.

ABQ47102;

12-JUL-2002 (first entry)

Oligonucleotide for detecting cytosine methylation SEQ ID NO 33693.

Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

Homo sapiens.

WO200218632-A2

07-MAR-2002.

01-SEP-2001; 2001WO-EP10074.

01-SEP-2000; 2000DE-1043826 05-SEP-2000; 2000DE-1044543

T-40000 10002-348-60

(EPIG-) EPIGENOMICS AG.

Olek A, Piepenbrock C, Ber

K, GuetigoD;

Berlin

WPI; 2002-371829/40.

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated (C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonuclectides and/or peptide-nucleic acid (PNA) cligoners and the degree of hybridisation to both classes is determined from the label on the amplicon, then the ratio of labels hybridised to the two classes of oligoners, the degree of methylation is calculated. The method is used: (1) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovaccular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleocide

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This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C. to uracial, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two classes of oligomers, the degree of methylation is calculated. The method is used: (i) for dagnosis and/or prognosis of side effects of themethod is used: (i) for dagnosis and/or prognosis of side effects of themethod is used: (i) for dagnosis and/or prognosis of side effects of the method is used: (i) for dagnosis and/or prognosis of side effects of collior respective confinement of systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (ii) for differentiation of cell or tissue
        types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ5411 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis; comprises selective hybridization of amplicons from chemically treated DNA -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, cytosine methylation, 5'-CpG-3', uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism;
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                 Query Match 2.0%; Score 21; DB 24; Length 755;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 21; Conservative 0; Mismatches 0; Indels
  for differentiation of cell
                                                                                                                                               Sequence 755 BP; 125 A; 78 C; 282 G; 270 T; 0 other;
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SNP; cell differentiation; ds
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; cytokine; cell proliferation; cell differentiation; growth factor;
ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                                                                                      2.0%; Score 21; DB 24; Length 755; 00.0%; Pred. No. 5;
                                                                                                                                                                                                                                                                                                  0; Indels
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                                                                                                                                                     Sequence 755 BP; 270 A; 282 C; 78 G; 125 T; 0 other;
                                                                                                                                                                                                                  Query Match 2.0%; Score 21; DB Best Local Similarity 100.0%; Pred. No. 5; Matches 21; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                   438 AAAATCCCGACGACGACGAA 458
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:D ABA08516 standard; cDNA; 453 BP.
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27-APR-2000; 2000US-0560875.
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P-PSDB; ABB11272.
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the control activities, including cytokine, cell proliferation or cell differentiation activities stem cell growth factor activity; immunomodulatory activity; activing respect activity; activing activity; activing activity; activing activity; activing activities activities, activity; activing activities, thrombotic or thrombotic or chemokinetic activities; haemostatic, thrombotic or thrombotic or activities; activities; normal because the involved in oncogenesis, cancer cell proliferation or metastasis.

Completed in oncogenesis, cancer cell proliferation or metastasis or manipulation are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy; Such conditions include cancers, haematopoletic disorders (e.g., myeloid or lymphoid cell conditions, e.g., by protein or gene therapy; Such conditions include cancers, baematopoletic disorders (e.g., myeloid or lymphoid cell disorders), chronic inflammatory conditions (e.g., asthma or arthritis), proliferative retinopathy, atherosclerosis, coronary heart disease, arterial ischaemia, bone disorders (e.g., osseoporosis), and abnormal vascular growth. Polypeptides involved with tissue regeneration and carefal infections and ulcers), while those with immunomodulatory activities may be used to promote even cell growth. For example, such polypeptides may be used to promote cell growth. For example, such polypeptides may be used to used to culture to give rise to neurospithalial cells that can be used to augment or replace cells damaged by illness, and indicing and also be used to the above conditions, and indicing and indicing and also be used to be augment or replace cells damaged by illness, and indicing and also be used to the above conditions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                screening techniques. The present sequence represents a cDNA encoding novel human polypeptide of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 20; DB 22; Length 453;
Pred. No. 16;
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100.04; Pred. No. 10....
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99US-0123548.
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99US-0126264.
99US-0126785.
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99US-0128234.
99US-0128714.
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99US-0130077.
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Matches 20, Conservative
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PR 24-AUG-1999 9908-

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                                                                                                                                                                                                                                                                                                   1.8%; Score 19; DB 21; Length 416;
100.0%; Pred. No. 50;
ive 0; Mismatches 0; Indels
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AC36816
D AAC36816 standard; DNA; 499 BP.
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99US-0160814.
99US-0160881.
99US-0161404.
99US-0161406.
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                                                                                                                                                                                                                                                                                                              Local Similarity 100.
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09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
01-APR-1999;
06-APR-1999;
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16-APR-1999;
19-APR-1999;
21-APR-1999;
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Best Local S
Matches 19
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The method
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA
                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Oligonucleotide for detecting cytosine methylation SEQ ID NO 30293
                                                                                                                                                                                                                                                                       .
0
                                                                                                                                                                                                                                       DB 21; Length 499;
49;
                                                                                                                                                                                                                                                                     0; Indels
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                                                                                                                                                                                                                                       Ouery Match

1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                  553 TCCTCCGGTTTAGCTCCAA 571
                                                                                                                                                                                                                                                                                                                              87 rccrccccrrraccrccaa 105
                                                                                                                                                                                                                                                                                                                                                                      RESULT 9
ABQ43702/c
ID ABQ43702 standard; DNA; 600 BP.
99US-0160814.
99US-0160915.
99US-0160981.
99US-0160981.
99US-0161404.
99US-0161406.
99US-0161359.
99US-0161359.
99US-0161359.
99US-0161359.
99US-0161359.
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05-SEP-2000; 2000DE-1044543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-2002 (first entry)
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28-OCT-1999;
29-OCT-1999;
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is used: (i) for diagnosis and/or prognosis of side effects of therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's); and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many C residues to be determined simultaneously. ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.

Sequence 600 BP; 136 A; 53 C; 216 G; 195 T; 0 other;

24; Length 600; 0; Indels Score 19; DB 2 Pred. No. 49; 0; Mismatches 1.8%; Scor. 100.0%; Pre 441 AATCCCGACGACGACGAAC 459 Query Match
Best Local Similarity 100...
Best Local Similarity 100... ≿

Gaps

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238 AATCCCGACGACGACGAAC 220 ਖ਼

ABQ43703 standard; DNA; 600 ESULT 10 ABQ43703

ABQ43703;

(first entry) 12-JUL-2002 Oligonucleotide for detecting cytosine methylation SEQ ID NO 30294.

numan; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis; drug; side effect; cancer; central nervous system; cardiovascular; gastrointestinal; respiratory system; single nucleotide polymorphism; SNP; cell differentiation; ds.

sapiens Ношо

WO200218632-A2

77-MAR-2002

01-SEP-2001; 2001WO-EP10074

01-SEP-2000; 2000DE-1043826, 05-SEP-2000; 2000DE-1044543,

(EPIG-) EPIGENOMICS

Olek A, Piepenbrock C,

WPI; 2002-371829/40.

Guetig

Berlin K,

Determining the degree of cytosine methylation in genomic DNA, useful for diagnosis and prognosis, comprises selective hybridization of amplicons from chemically treated DNA

Claim 12; 56pp + Sequence Listing; 56pp; German.

This invention describes a novel method for determining the degree of methylation of a particular cytosine in a motif 5'-CpG-3', present in a genomic sample of DNA. The sample is treated chemically to convert cytosine (C) but not methylated C, to uracil, then part of the genomic DNA that contains the target C is amplified to form a labeled amplicon. The amplicon is hybridised to two classes, each with at least one member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers and the degree of hybridisation to both classes is determined from the label on the amplicon. From the ratio of labels hybridised to the two lasses of oligomers, the degree of methylation is calculated. The method is used: (i) for diagnosis and/or prognosis of side effects of the reapentic drugs and of a wide range of diseases, e.g. cancer, disorders of the central nervous, cardiovascular, gastrointestinal and respiratory

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systems etc., particularly by detecting mutations or single nucleotide polymorphisms (SNP's), and (ii) for differentiation of cell or tissue types and for investigating cell differentiation. The method allows the methylation status of many c residues to be determined similtaneously. ABQ13411-ABQ84121 represent genomic DNA sequences used to illustrate the method for determining the degree of cytosine methylation described in the disclosure of the invention.
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                                                                                                                                                   Score 19; DB 24; Length 600;
Pred. No. 49;
                                                                                                                                                                                   0; Indels
                                                                                                                    Sequence 600 BP; 195 A; 216 C; 53 G; 136 T; 0 other;
                                                                                                                                                   Query Match
1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 49;
Matches 19; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                              Human secretory polymucleotide (sptm) 161.
                                                                                                                                                                                                              441 AATCCCGACGACGACGAAC 459
                                                                                                                                                                                                                                         363 AATCCCGACGACGACGAAC 381
                                                                                                                                                                                                                                                                                                                    ВР
                                                                                                                                                                                                                                                                                                                 ABL99906 standard; cDNA; 908
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ABL99906/c
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                                                                                                                                                                               Stuart J, Lincoln SE, Altus CM, Dufour GE, Chalup MS, Hillman JL, Jones AL, Yu JY, Wright RJ, Gietzen D, Liu TF, Yap PE, Dahl CR; Momiyama MG, Bradley DL, Rohatgi SD, Harris B, Roseberry AM; Peralta CH, David MH, Panzer SR, Flores V, Daffo A; Marwaha R, Chen AJ, Chang SC, Au AP, Inman RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Polynucleotide sequences encoding human secretory proteins useful for gene therapy of e.g. genetic deficiency disorders, cancers, and diseases caused by intracellular parasites
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Best Local Similarity 100.0%; Pred. No. 48;
Matches 19; Conservative 0; Mismatches 0; Indels 0
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07-SEP-2000, 2000US-230951P.
07-SEP-2000, 2000US-231163P.
07-SEP-2000, 2000US-231832P.
                                                                                                                      (INCY-) INCYTE GENOMICS INC.
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99US-0123180.
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P-PSDB; ABB97909.
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05-MAR-1999;
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99US-0134256.
99US-0134218.
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99US-0140991.
99US-0141842.
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99US-0142154.
99US-0142055.
99US-0142803.
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99US-0134370.
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99US-0135124.
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15.-UL-1999; 99US-0144005.

R 16-UL-1999; 99US-014408.

R 19-UL-1999; 99US-0144125.

R 19-UL-1999; 99US-0144131.

R 19-UL-1999; 99US-0144131.

R 20-UL-1999; 99US-0144131.

R 20-UL-1999; 99US-0144131.

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R 20-UL-1999; 99US-0144131.

R 21-UL-1999; 99US-0144131.

R 22-UL-1999; 99US-0144131.

R 22-UL-1999; 99US-014508.

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R 11-AUG-1999; 99US-014308.

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1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 47;
Matches 19; Conservative 0; Mismatches
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9908-0158323-9908-0158369-9908-0158369-9908-0159329-9908-0159329-9908-0159331-9908-0159638-9908-015968-9908-0160815-9908-016098-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-0160989-9908-01
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990S-0123180.
990S-012548.
990S-0125788.
990S-0126785.
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99US-0161360.
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25-0CT-1999;
25-0CT-1999;
25-0CT-1999;
26-0CT-1999;
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AAC43180
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Human; ss; gene; secretory protein; secretory polynucleotides; SPTM; SPTM: Servar-telad disease; somatic gene therapy; germline gene therapy; servar lated disease; somatic gene therapy; germline gene therapy; servar combined immunodeficiency; intracellular parasite protection; fungal parasite; protozoan parasite; cell proliferative disorder; cancer; makinson's disease; metror neuron disorder; ADS; neurological disorder; parkinson's disease; mentor neuron disorder; prion disease; cerebral pals; dernetomyceitis; prion disease; cerebral pals; dernetomyceitis; polymycsitis; morphycath nervous system disorder; mental disorder; Pourette's syndrome.
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BL99921/c
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The invention comprises the amino acid and coding sequences of human secretory (SPTM) proteins. The SPTM DNA and amino acid sequences are useful for treating a disease or condition associated with the expression of functional SPTM. The SPTM DNA sequences are useful for somatic or germline gene therapy to correct a genetic deficiency (e.g. severe combined immunodeficiency). The SPTM DNA sequences are also useful in parasites and protoccan parasites). The SPTM DNA and protein sequences are also useful in parasites and protoccan parasites). The SPTM DNA and protein sequences are also useful for diagnosing cell proliferative disorders, cancer, immune disorders (e.g. AIDS), neurological disorders (e.g. Fungal sclesses), motor neuron disorders, demyelinating diseases (e.g. multiple sclerosis), meningitis, abscesses, prior diseases (e.g. multiple sclerosis), and polymyositis, myosethenia gravis, and mental disorders (e.g. Tourette's syndrome). CDNA sequences ABL99229
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Dahl CR;
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06-SEP-2000; 2000US-230865P
06-SEP-2000; 2000US-230988P
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07-SEP-2000; 2000US-231832P
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P-PSDB; ABB97925.
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26-MAR-2002 (first entry)

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher enkaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention addiscloses genomic DNA sequences (ABLi6176-ABL30511), expressed DNA sequences (ABLi6175) and the encoded proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cell interactions -
Drosophila melanogaster expressed polynucleotide SEQ ID NO 37076.
                                                                Drosophila; developmental biology; cell signalling; insecticide; pharmaceutical; gene; ss.
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P-PSDB; ABB70095.
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Search completed: February 2, 2004, 03:13:24 Job time : 317.239 secs

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0; Gaps

0; Indels

1.8%; Score 19; DB 100.0%; Pred. No. 40; cive 0; Mismatches

Query Match
Best Local Similarity 100.
Matches 19; Conservative

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		mean lin	cophyta, Embry tophyta, Embry dicctyledons ssicaceae, Ara Focks, N. Gin rogge, J. and rogge, J. and rogge, J. and rogge, J. and rogge, J. and ar boohydra ar Biology e University,
10000000000000000000000000000000000000	BB145694 BB134002 BB134002 BB49424 BX66337 BX676112 BX683191 BX583191 BX363191 BX363191 BX363191 BX363191 BX36214 A1795304 A1795304 A1795304 A1795304 A1795304 A1795304 A1795304 A166367	BH6170 AZ2130 BH6772 BH6572 BH6494 AA64444 CB6996 CB7953 ALIG	(thale criticals) Streintae; Streintae; Streintae; Brown, T. J. J. J. J. J. J. J. J. J. J. J. J. J.
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es 320; Conservative
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Arabidopsis thaliana
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantas; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
1 (bases II) Brassicales; Brassicaceae; Arabidopsis.
Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M., Oono,Y., Sakurai,T., Carninci,P., Kawai,J., Itoh,M., Ishii,Y., and Shinozaki,K.
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Fax: 517 353 9334

Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Michigan State University 309 Botany
Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGCCGTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACGATGGCTAGACCACCTCCTT 835
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 31.2%; Score 334; DB 10; L
Best Local Similarity 100.0%; Pred. No. 6.9e-174;
Matches 334; Conservative 0; Mismatches 0;
                                                                                                                                                            /organism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/clone="M28F8"
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Plant Functional Genomics Research Group
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AV825375.1 GI:19867435
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

DEFINITION

RESULT 2 AV825375 LOCUS

ò DP.

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73.1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan Teli 81-298-36-4369
Fax: 81-298-36-9660
Email: mseki@rtc.riken.go.jp
An Arabidopals full-length CDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and SalI. This clone is in a modified Daluescript vector. Please visit our web site (http://www.gsc.riken.go.jp/e/plant/index _e.html) for further
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   378 bp mRNA linear BST 19-MAR-2001
Clone M31B6 5', mRNA sequence.
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edons; core eudicots; rosid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 cccacagragactrogagcccaaggccgagccggraargccgragacgrrrrcaargrcrrra
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/note="Site_1: BamH1; Site_2: Sal1; subjected
cold-treated (1, 2, 5, 10, 24 h7)"
118 c 117 g 117 t 3 others
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, T.
Spermatophyta, Magnoliophyta, eudicotyledons, core eud.
; eurosids II; Brassicales, Brassicaceae, Arabidopsis, (bases 1 to 378)
White, J. A., Todd, J., Newman, T., Focks, N., Girke, T., Ma.
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                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Arabidopsis thaliana"
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/clos="RAFI07-08-P04"
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100.0%; Pred. No. 4.5e-166;
iive 0; Mismatches 0;
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Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Bagnoliophyta, eudicotyledons, core endicots; rosids; eurosids II, Brassicales; Brassicaceae, Arabidopsie.

(bases 1 to 335)
Newman,T., deBruijn,F.J., Green,P., Kēegstra,K., Kende,H., McIntosh,L., Ohrogge,J., Raikhel,N., Somerville;S., Thomashow,M., Retzel E. and Somerville,C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones Plant Physiol. 106, 1241-1255 (1994).
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                                                                                                                                                                                                                                      /clone lib="Gif-Seeda"
/note="Vector: Lambda ZAPII non-oriented; Physiological
condition: greenhouse plants. tissue_type: Green siliques
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 GCCACGIGIGGGGCTAGGATTTTTCAATTAACTCGAGAGTTAGGTCACAAATCCGACGGC 250
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Contact: Berthomieu P., Guerrier D., Giraudat J.
Genetique Moleculaire d'Arabidopsis
ISV - UPRO, CNRS
Avenue de la Terrasse,1198 Gif-sur-Yvette Cedex,France
Email: Giraudat@cnrs-gif.fr.
1.0cation/Qualifiers
1.388
                                                                                                                                                                                                                                                                                                                                                                                      Length 388;
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100.0%; Pred. No. 9.6e-113;
:ive 0; Mismatches 0;
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MSU-DOE Plant Research Laboratory
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Fax: 517-353-9168
Email: 22313tcm@ibm.cl.msu.edu
Seg primer: T7 dye primer.
1. 335
                                                                                                                                                                      /mol_type="mRNA"
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                                                                                                            FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
                                                               Contact: Benning, C
Debt. of Blochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           235068 18-JUL-1994
ATTS3707 Gif-Seeda Arabidopsis thaliana cDNA clone YAY344 5', mRNA
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                                                                                                                                                       , USA

Fax: 517 355 1609

Fax: 517 353 9334

Email: benning@msu.edu

Michigan State University DNA Sequencing Facility Arabidopsis

Biological Resource Center, The Ohio State University, 309 Botany

Zoology Bldg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: (12929371.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   103 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GATCTAACCATCATCAACGGCGTCAGAAACGTCGAAAACTTCAAGACCTTTCCAAGTAAAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTCAATGTCTTTA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="seed"
/dev_stage="5-13 days after flowering"
/dev_stage="5-13 days after flowering"
/lab host="8.coli"
/clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: pBluescript SK-;
/note="Organ: Site_2: XhoII"
-97 c 81 g 92 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GATCTAACCATCATCAACGGGGTCAGAAACGTCGAAACTTCAAGACCTTTCAAGTAAAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.8%; Score 244; DB 10; L
Best Local Similarity 100.0%; Pred. No. 7.3e-124;
Matches 244; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                  organism="Arabidopsis thaliana"
    (4), 1582-1594 (2000)
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Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                 db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                         location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                        /mol_type="mRNA"
/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     clone="M31B6'
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    Plant Physiol, 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         244
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survey sequence.
BH450567
BH450567.1 GI:176
GSS.
                                                                                                                                                   Query Match
Best Local Similarity
Matches 38; Conservat
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BH450567/c
LOCUS
DEFINITION
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BH511920/c
                                                                                    BASE COUNT
ORIGIN
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Brassica oleracea
Brassica oleracea
Brassica oleracea
Brassica oleracea
Bukaryora, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; endicotyledons; core endicots; rosids;
; eurosids II; Brassicales; Brassicacee; Brassica.

El (bases 1 to 586)

Stati,M., O'Shauphnessy,A., Palmer,L., Bahret,A., Baker,J., Balija
V., Cunnius,D.M., Katenberger,F., King,L., Kirchoff,K., Kuit,K.,
Miller,B., Muller,S., Mascimento,L., Preston,R., Santos,L.,
V., Cutavern,T., Dedhia,N., Rabinowicz,P.D. and McCombie,W.R.
Whole Genome Shorgun Reads from Brassica oleracia (2002b)
Unpublished
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
Tel: 516 367 8884
Email: mccombie@cshl.org
Plate: gt27 row: g column: 10
              // mol_type="mrnna" |
// mol_type="mrnna" |
// mol_type="mrnna" |
// dlone="lab="laxon:3702" |
// dlone="lab="lambda="PRL2" |
// dlone="lab="lambda="PRL2" |
// dlone="lab="lambda="PRL2" |
// note=""Vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not; lambda PRL2 is a cDNA library derived from equal quantities of 4 pools of mRNA. The maxNA sources were 1) 7 day germinated etiolated seedlings; 2) tissue culture grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark- rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cDNA. " 13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone_lib="BoBudsol"
hote="Vector: M13 for .x reads, pBluescript for .b and .g
reads; Site 1: EcoRV; Whole genome shotgun library from
flowering buds. DNA was purified from a crude nuclear prep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA linear GSS 25-FEB-2002 gt27q10.g1 BoBuds01 Brassica oleracea genomic clone gt27g10 5', BH21111.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     40 rcaaacrcraagagccgrrgarcraaccarcarcacgcgrcaaaggrcgaaacrrc 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCAAACTCTAAGAGCCGTTGATCTAACCATCAACGGCGTCAGAAACGTCGAAACTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  102 AAGACCTTTCCAAGTAAATCCCACAGTGAGTCTCGAGCCCAAGGCGGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    10.1%; Score 108; DB 14;
.larity 100.0%; Pred. No. 2.7e-48;
Conservative 0; Mismatches 0;
'organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
/db_xref="taxon:3712"
/clone="gt27g10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              High quality sequence stop: 586.
Location/Qualifiers
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BH741132.1 GI:18875745
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                                                                                                                                                                                                                                                                                                                                                                                                                                         al Similarity
108; Conserv
                                                                                                                                                                                                                                                                                                                                                     96
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Best Local S
Matches 108
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3H741132/c
COCUS
SEINITION
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Brassica oleracea
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids
; eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 798)
Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.
Wholbished
Oupublished
Other_GSSs; BOHGA14TR
                                                                                                                                                                                                                                                                                                                                                                                                                                      BH511920 798 bp DNA linear GSS 13-DEC-2001
BOHGA14TF BOHG Brassica oleracea genomic clone BOHGA14, genomic
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241, genomic
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using Brassica oleracea TO1000DH3 buds provided by Thome Osborn at the University of Wisconsin. Genomic DNA provided by Pablo Rabinowicz (CSHL) and shotgun library prepared in McCombie Lab."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="BOHG"
/note="Vector: pH081, Site_1: BatXI, 2-3 kb sheared
genomic DNA inserted into pH0S1 using BstXI linkers"
210 c 225 g 202 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: 301-838-3523
Fax: 301-838-0208
Email: cdccwn@t.gr.org
DNA is from a doubled haploid provided by Tom Osborn.
Class: sheared ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 798;
                                                                                                                                                                         Length 586;
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9712 Medical Center Drive, Rockville, MD 20850, USA.
                                                                                                                                                                                                                    0; Indels
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                                                                                                                                                                                                                                                                    262 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTT 299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3.5%; Score 38; DB 28; I 100.0%; Pred. No. 2.8e-09; iive 0; Mismatches 0;
                                                                                                                                                                      Score 38; DB 28; I
Pred. No. 2.6e-09;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                  41 AGGATACGGATGCCTGCCACGTGTGCGGCTAGGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Coation Qualifiers
1.798
/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:3712"
/clone="BOHGA14"
                                                                                                                                                       3.5%; Scc...
100.0%; Pred
0; N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Burvey sequence.
BH511920
BH511920.1 GI:17720010
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Chris Town
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity 100.
Matches 38; Conservative
                                                                                                                                                                                                                      Conservative
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Gape

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AN092131 318 bp mRNA linear EST 18-MAY-2001 EST285227 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA colone cLET17P7, mRNA sequence.
/db_xref="taxon:3712"
/clone="BOHTGS8"
/clone lib="BO 2 3 KB"
/note="Vector: PHOS1; Site_1: BetXI; 2-3 kb sheared
ynote="Vector: PHOS1; Site_1: BetXI linkers"
1 126 c 160 g 155 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
5 prime sequence.
Location/Qualifiers
                                                                                                                                                                                                                               ch 3.0%; Score 32; DB 28; Length 600; I Similarity 100.0%; Pred. No. 5.6e-06; 32; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24; DB 9; Length 318; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pred. No. 0.13; Pr
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/mol type="mRNA"
collivar="Rio Grande PtoR"
/db xref="taxon:4081"
/clone="clET17P7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,J.
Generation of BSTs from tomato leaf tissue
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Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW092131.1 GI:6057642
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ORGANISM
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                                 Brassica oleracea

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids

i eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 656)

Town, C.D., Van Aken, S., Utterback, T., Koo, H. and Fraser, C.M.

Wholb egenome shotgun sequencing of Brassica oleracea

Unpubblished

Other_GSSs: BOGDQ41TF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                600 bp DNA linear GSS 20-FEB-2002 BOHTG58TR BO 2 3 KB Brassica oleracea genomic clone BOHTG58, BH71s.ca survey sequence.
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Brassica oleracea
Brassica oleracea
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Brassica.
1 (bases 1 to 600)
Town.C.D., Van Aken,S., Utterback,T., Koo,H. and Fraser,C.M.
Whole genome shotgun sequencing of Brassica oleracea
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/clone="BOGDQ41"
/clone=1bb="BOGD;
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
/note="Vector: pHOS1; Site_1: BstXI; 2-3 kb sheared
genomic DNA inserted into pHOS1 using BstXI linkers"
167 c 190 g 157 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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0
                                                                                                                                                                                                                                                                                                                                              Tel: 301-838-3523
Fax: 301-838-3523
Fax: 301-80286
DNA is from a doubled haploid provided by Tom Osborn. Seq primer: TR
Class: sheared ends.
Location/Qualifiers
1...656/
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DNA is from a doubled haploid provided by Tom Osborn.
Seg primer: TR
Class: sheared ends.
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100.0%; Pred. No. 1.2e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    563 GCCGCCACGGGTACGGGAACGGTTCCCGCCATCGC 529
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/organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Brassica oleracea"
/mol_type="genomic DNA"
/strain="TO1000DH3"
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Contact: Chris Town
                                                                                                                                                                                                                                                                                             Contact: Chris Town
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Fax: 301-838-0208
            Brassica oleracea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Best Local Similarity
Matches 35; Conserv
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TITLE
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TITLE
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JMMENT
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H735681
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Gapa

CCESSION TERSION TEYWORDS OURCE ORGANISM

OCUS

11775374

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/clone lib="tomato mixed elicitor, BTI"
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/nots="Vector: pBlueScript SK(-); Site_1 = response
/nots; cLET - Inoculated with a variety of disease response
elicitors: Plants exposed to 2,6 dichloroison.cotinic
acid, BTH, jamonic acid, ethylene, fenthion, EIX,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Lycopersicon esculentum
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
asterids; lamiids; Solanales; Solanaceae; Solanum; Lycopersicon.
1 (bases 1 to 642)
1 Ascenzo, M., He,X., Lyman, J., Holt, I.B., Liang, F., Upton, J.,
Ronning, C.M., Craven, M.B., Fujii, C.Y., Bowman, C.L., Nierman, W.,
Fraser, C.M., Venter, J.C., Martin, G.B., Tanksley, S.D. and Glovannoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: DBlueScript SK(-); Site_1: EcoR1; Site_2: Xho1; cLBR - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5. end with EcoR1 and 3. end with XhoI site."
                                                                                                                                                                                                                           1. .610 "Acopersicon esculentum" |
|/organ.lnycopersicon esculentum" |
| /mol.type="mRNA" |
| /mol.type="mRN1-12 (35S::Pto in Rio Grande x Money Maker) "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              642 bp mRNA linear EST 18-MAY-20.
EST2838880 tomato mixed elicitor, BTI Lycopersicon esculentum cDNA AW041016
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                         Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Qualifiers
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Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2.2%; Score 24; DB 9; Length 610;
100.0%; Pred. No. 0.16;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cornell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | forganism="Lycopersicon esculentum" | fmc| type="mRNA" | fculfivat="RNA fro Grande PtoR" | fculfivat="taxon:4081" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="clET6G21" | fclone="
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dev stage="4-6 week old plants"
lab_host="XL1-Blue MRF'"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      clone lib="tomato resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="leaf"
/dev_stage="4-week_old"
/lab_host="SOLR"
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/clone="cLER1A9"
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/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
/note="Vector: pBlueScript SK(-); Site_1: EcoR1; Site_2:
Divot: CLER - Tomato Pseudomonas Resistant EST Library.
Directionally cloned cDNAs inserted into pBlueScript SK(-) at 5; end with EcoR1 and 3; end with XhoI site."
114 c 110 g 148 t
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Generation of ESTs from Pseudomonas resistant tomato
                                                                                                                                                                                                                                                Lycopersicon esculentum (tomato)
Lycopersicon esculentum
Eukaryota, Viridiplantee, Streptophyta, Embryophyta, Tracheophyta,
Eukaryota, Wagnoliophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; soulicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaces; Solanum, Lycopersicon.
1 (bases 1 to 481)
D' Ascenzo,M., He,X., Lyman,J., Matern,A.L., Vision,T., Holt,I.E.,
Liang,F., Upton,J., Ronning,C.M., Craven,M.B., Fulii,C.Y., Bowman,
C.L., Nierman,W., Fraser,C.M., Venter,J.C., Tanksley,S.D.,
Glovannoni,J.J. and Martin,G.B.
Generation of ESTs from Pseudomonas resistant tomato
                                      EST 18-MAY-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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/mol_type="mRNA"
/cultivar="HL12" (358::Pto in Rio Grande x Money Maker)"
/db_xref="taxon:4081"
/clone="cleR15G18"
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EST249484 tomato resistant, Cornell Lycopersicon esculentum cDNA
A1484214
                             AI775374 tomato resistant, Cornell Lycopersicon esculentum cDNA clone cERR15G18, mRNA sequence.
AI775374 GI:5273415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html
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/dev_stage="4-week_old"
/lab_host="SOLR"
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BB042901 GI:8449287
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
asterids; lamids; Solanales; Solanaceae; Solanum; Lycopersicon.

(bases 1 to 670)
van der Hoeven, R., Bezzerides, J., Sun, H., Cho, J., Utterback, T.,
Hansen, C., Ronning, C. and Tankeley, S.
Generation of ESTs from tomato shoot/meristem tissue
Unpublished
okadaic acid, or systemin prior to tissue harvest. EcoRI site was destroyed during cloning."
144 c 141 g 199 t lothers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="Vector: pBluescript SK(-); Site_1: EcoR1; Site_2: Xho1; Small expanding leaves from the growing tip were taken from greenhouse plants (4-6wks old TA496). Tissue was immediately frozen in liquid nitrogen."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /tissue_type="shoot/meristem"
[dev_stage="developing shoots from 4-6wks old plants"
/lab_host="golk"
/clone_lib="tomato shoot/meristem"
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Contact: CUGI
Clemson University
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Email: http://www.genome.clemson.edu/orders/index.html.
Location/Gualifiers
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Pred. No. 0.16;
                                                                                                    Length 642;
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/mol_type="mRNA"
/cultivar="TA496"
                                                                                                    DB 9;
0.16;
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clone="cTOF28K14"
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ERROR Inhearpote, Messes a) Cooledges (Cantalate, Variaberes; Excledescend); Mammalia Butheria; Rodentia; Sciincgmath; Muridae, Murinae, Mus. Thoses 1 Co. 223)

Konno, Alazawa, X., Akahira, S., Akiyama, J., Arakawa, T., Carrinci, Y., Endo, T., Pakuda, S., Milana, S., Akiyama, J., Arakawa, T., Carrinci, I., E., Endo, T., Pakuda, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, S., Milana, M., Matana, M., Oda, H., Okazahi, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M., Matana, M.,
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ORIGIN

0; Gaps Query Match 2.1%; Score 23; DB 10; Length 222; Best Local Similarity 100.0%; Pred. No. 0.41; Matches 23; Conservative 0; Mismatches 0; Indels

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Search completed: February 2, 2004, 05:01:17 Job time : 2490.95 secs

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NESON-345-882-1

Sequence 1, Application US/09345882

Sequence 1, Application US/09345882

Parent No. 6399373

GENERAL INFORMATION:

APPLICANT: Bougneleret, Lydie

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOWA BINDING PROTEIN (RBP-7)

TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOWA BINDING PROTEIN (RBP-7)

TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.

FILE REFERENCE: GENSET.031A

CURRENT FILING DATE: 1999-06-30

PRIOR FILING DATE: 1998-06-30

PRIOR FILING DATE: 1998-12-10

NUMBER OF SEQ ID NOS: 140

SOFTWARE: Patent.pm

SOFTWARE: Patent.pm

SENOTING 1

LENOTH: 162450

TYPE: DNA
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Patent No. 6492343
GENERAL INFORMATION:
APPLICANT: Tikco, Suresh
APPLICANT: Tikco, Suresh
APPLICANT: Tikco, Suresh
APPLICANT: Babiuk, Lorne
APPLICANT: Babiuk, Lorne
APPLICANT: Babiuk, Lorne
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
CURRENT APPLICATION NUMBER: US/09/292,034
CURRENT FILIG DATE: 1999-04-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PASLSEQ for Windows Version 3.0
SEQ ID NO 1
LENGTH: 34094
                                                   -09-328-352-1768
                                               US-09-328-352-1768
US-09-364-206-5
US-09-364-206-5
US-07-81-7038-9
US-08-184-236-9
US-08-184-236-9
US-08-407-4108-9
US-08-485-500-9
PCT-US91-02370-9
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Pred. No. 4;
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1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 44;
Matches 19; Conservative 0; Mismatches
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FEATURE:
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Sequence 1, Appli
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           GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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US-09-328-352-186

US-08-510-878-3

US-09-252-991A-6792

US-09-155-991A-6792

US-09-155-940-1

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US-08-444-818-143

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Gapop_60.0 , Gapext 60.0
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                                                                                                                                            ION: 90842
INFORMATION: 99-1437-325
                                                                                                                                                                                                                                               ATION: 97122
HER INFORMATION: 99-1442-224
                                                                                                                                                                                                                                                                                                      ION: 97152
INFORMATION: 5-129-144
                                                                PEATURE:
WAME/KEY: allele
WOCATION: 88073
OTHER INFORMATION: 5-127-261
                                     GCCATION: 72794
THER INFORMATION: 5-124-273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WE/KEY: allele
CATION: 108106
HER INFORMATION: 5-135-155
                                                                                                                                                                                                                                                                                                                                          ME/KEY: allele
CATION: 99098
HER INFORMATION: 5-130-257
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATION: 103806
ER INFORMATION: 5-131-395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CATION: 108149
HER INFORMATION: 5-135-198
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OCATION: 108308
THER INFORMATION: 5-135-357
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OCATION: 134134
THER INFORMATION: 5-140-120
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NAME/KEY: allele
NOCATION: 134362
OTHER INFORMATION: 5-140-348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5-133-375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION: 5-136-174
                                                                                                                                                                                 AME/KEY: allele
OCATION: 93714
THER INFORMATION: 5-128-60
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LOCATION: 146328
OTHER INFORMATION: 5-143-84
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ME/KEY: allele
)CATION: 106940
]HER INFORMATION:
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OCATION: 134374
THER INFORMATION:
                          NAME/KEY: allele
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NWE/KEY: allele
OCATION: 90819..90865
THER INFORMATION: complement polymorphic fragment 99-1437-325 SEQ ID49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ME/KEY: allele
CATION: 90819..90865
HER INPORMATION: complement polymorphic fragment 99-1437-325 SEQ ID70
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OCATION: 97099. 97145
THER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OCATION: 97099..97145
THER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID50
                                                                                                                                                                                                                                                                                        OCATION: 72771..72817
THER INFORMATION: polymorphic fragment 5-124-273 SEQ ID30
                                                                                                                                                                                                                                                                                                                                                  AME/KEY: allele
OCATION: 72771...72817
THER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AME/KRY: allele
OCATION: 88050. 88096
THER INFORMATION: polymorphic fragment 5-127-261 SEQ ID52
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LOCATION: 97130..97177
JTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KRY: allele
LOCATION: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
FEATURE:
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JAME/KEY: allele
JOCATION: 88050..88096
OTHER INFORWATION: polymorphic fragment 5-127-261 SEQ ID31
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JOCATICN: 99075..99121
OTHER INFORMATION: polymorphic fragment 5-130-257 SEQ ID34
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THER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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INFORMATION: polymorphic fragment 5-128-60 SEQ ID32
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OCATION: 93690. 93736
THER INFORMATION: polymorphic fragment 5-128-60 SEQ ID53
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                                            : polymorphic base
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                                                                                                                                                                                                                          polymorphic
                                                                                                                                   : polymorphic
AME/KEY: allele
OCATION: 146345
THER INFORMATION: 5-143-101
                                                                                                                                                                         NAME/KEY: allele
LOCATION: 160031
OTHER INFORMATION: 5-148-352
                                                                                  WAME/KEY: allele
LOCATION: 150329
DTHER INFORMATION: 5-145-24
FEATURE:
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AME/KEY: allele
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AME/KEY: allele
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OTHER INFORMATION: n equals a, t, c, or g
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OTHER INFORMATION: n equals a, t;
                              LOCATION: (84773)... (84773)

OTHER INFORMATION: n equals a, t, NAME/KEX: misc feature
LOCATION: (84808)... (84808)

OTHER INFORMATION: n equals a, t, NAME/KEX: misc feature
LOCATION: (84812)... (84812)

OTHER INFORMATION: n equals a, t, NAME/KEX: misc feature
LOCATION: (98120)... (98120)

OTHER INFORMATION: n equals a, t, NAME/KEX: misc feature
LOCATION: (98159)... (98129)

OTHER INFORMATION: n equals a, t, NAME/KEX: misc feature
LOCATION: (98239)... (98239)

OTHER INFORMATION: n equals a, t, NAME/KEX: misc feature
LOCATION: (98266)... (98266)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (98343)... (98343)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (103998)... (103998)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (148948)... (148948)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (148948)... (148948)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (148948)... (148948)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (148948)... (148948)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (148948)... (148948)

OTHER INFORMATION: n equals a, t, NAME/KEY: misc feature
LOCATION: (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (148948)... (1
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LOCATION: (309418).. (309418)
OTHER INFORMATION: n'equals a, t,
NAME/KEY: misc feature
LOCATION: (312837).. (312837)
OTHER INFORMATION: n equals a, t,
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LOCATION: (191995)..(191995)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
LOCATION: (231980)..(231980)
OTHER INFORMATION: n equals a, t
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LOCATION: (312993)...(312993)
OTHER INFORMATION: n equals a,
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LOCATION: (234814) .. (234814)
OTHER INFORMATION: n equals a,
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LOCATION: (309398)..(309398)
OTHER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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CTHER INFORMATION: n equals a, NAME/KEY: misc feature
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Patent No. 6503729
GARDEAL INFORMATION:
APPLICANT: Bult et al.
TITLE OF INVENTION: Complete Genome Sequence of the Methanogenic Archaeon, Methanococ
Patent No. 6503729
TITLE OF INVENTION: jannaschii
FILE REFERENCE: PB275
TITLE OF INVENTION NUMBER: US/08/916,421B
CURRENT APPLICATION NUMBER: US 60/024,428
PRIOR APPLICATION NUMBER: US 60/024,428
PRIOR PILING DATE: 1996-08-22
NUMBER OF SEQ ID NOS: 3
SOFTWARE: Patentin version 3.1
SEQ ID NO: 1
SEQ ID NO: 1
SEQ ID NO: 1
SEQ ID NO: 1
SEQ ID NO: 3
SOFTWARE: LENGTH: 1664976
TYPE: DAA
ORGANISM: Methanococcus jannaschii
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NAME/KEY: allele
LOCATION: 99094..99140
OTHER INFORMATION: polymorphic fragment 5-130-276 SEQ ID56
                                                                                                                                                                                                                                                   NAME/KEY: allele
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: allele
LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
NAME/KEY: allele
NAME/KEY: allele
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
FEATURE:
                                                                                                                    GX: allele
CN: 103783. 103828
INFORMATION: polymorphic fragment 5-131-395 SEQ ID36
                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: allele
LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
FRATURE:
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LOCATION: 106918..106966
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LOCATION: 108084..108130
OTHER INFORMATION: polymorphic fragment 5-135-155 SEQ ID59
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LOCATION: 108127..108177
OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID39
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1.7%; Score 18; DB 4
Best Local Similarity 100.0%; Pred. No. 13;
Matches 18; Conservative 0; Mismatches
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LOCATION: (28257)..(28258)
OTHER INFORMATION: n equals a,
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COCATION: (28222)
OTHER INFORMATION: n equals a,
NAME/KEY: misc_feature
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IS-08-916-421B-1/c
                                                                                             FEATURE:
NAME/KEY:
LOCATION:
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LOCATION: (1603734)..(1603734)
OTHER INFORMATION: n equals a, t, c, or NAVE/KEY: misc feature
LOCATION: (1637998)..(1637998).
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ION: (855539) . (855539)
INFORMATION: n equals a, t,
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INFORMATION: n equals a, t,
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INFORMATION: n equals a, t,
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LOCATION: (1313224)...(1313224)
OTHER INFORMATION: n equals a, t,
NAME/KEY: misc feature
LOCATION: (1349473)...(1349473)
OTHER INFORMATION: n equals a, t
NAME/KEY: misc feature
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MCATION: (779455)..(779455)
HER INFORMATION: n equals a,
                                                                                       NAME/KEY: misc feature
LOCATION: (657081)..(657081)
OTHER INFORMATION: n equals a,
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RMATION: n equals a,
INFORMATION: n equals a,
                                                                                                                                                          THER INFORMATION: n equals a, CAME/KEY: misco feature
                                                                                                                                                                                                                                                                                                                               OCATION: (713652)..(713652)
THER INFORMATION: n equals a,
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OCATION: (1130881)..(1130881)
THER INFORMATION: n equals a,
                                                     ION: (622708)..(622708)
INFORMATION: n equals a,
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THER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                             ION: (741684)..(741684)
INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ON: (779676)..(779676)
INFORMATION: n equals a,
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LOCATION: (1310998)..(1310988)
THER INFORMATION: n equals a,
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OTHER INFORMATION: n equals a,
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THER INFORMATION: n equals a,
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                                                                                                                                                  WAME/KEY: misc feature
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APPLICANT: Gary L. Breton et al.

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REPERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 186
LENGTH: 447
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                                                                                                           Query Match 1.7%; Score 18; DB 4; Length 1664976; Best Local Similarity 100.0%; Pred. No. 12; Matches 18; Conservative 0; Mismatches 0; Indels 0;
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1.6%; Score 17; DB 4; Length 447;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Vergion #1.30
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APPLICATION NUMBER: US/08/510,878
FILING DATE: 03-AUG-1995
                  ) NAME/KEY: misc feature

: DOCATION: (1664855)

: OTHER INFORMATION: n equals a, t, c,

US-08-916-421B-1
                                                                                                                                                                                                                          1522815 CAATGICTTTAGCTCCAC 1522798
                                                                                                                                                                                                                                                                                                     US-09-328-352-186
; Sequence 186, Application US/09328352
; Detent No. 6562958
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
PORGANISM: Acinetobacter baumannii
US-09-328-352-186
                                                                                                                                                                                      170 CAATGTCTTTAGCTCCAC 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          951 TTCATCGTCAATTGCAA 967
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REGISTRATION NUMBER: 32,181
REFERENCE/DOCKET NUMBER: 12
OTHER INFORMATION: n equals a,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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TELEPHONE:

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0; Mismatches
                                                                                  Application US/09252991A
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
, ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-6792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 CGGCGATTATAGCCGCC 387
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1.6%;
Best Local Similarity 100.0%;
Matches 17; Conservative 0
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Best Local Similarity 100.
Matches 17, Conservative
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                                                         -09-252-991A-6878
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APPLICANT: Yu, Fujio
APPLICANT: Yu, Fujio
APPLICANT: Yu, Fujio
APPLICANT: Yu, Fujio
TITLE OF INVENTION: A KANAMYCIN RESISTANCE GENE DERIVED FROM
TITLE OF INVENTION: MICROORGANISMS OF THE GENUS RHODOCOCCUS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Birch, Stewart, Kolasch and Birch
STREET: P.O. Box 747
CIIT: Falls Church
                                                                                                                                                                                                                                                                                   Length 516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 17; DB 1; Length 748;
                                                                                                                                                                                                                                                                                                                              0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/510,878
FILING DATE: 03-AUG-1995
CLASSIFICATION: 435
ATTCRNEY/AGENT INFORMATION:
NAME: Weiner, Marc S
REGISTRATION NUMBER: 32,181
REFERENCE/POCKET NUMBER: 124-121
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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Mismatches
                                                                                                                                                                                                                                                                       Query Match 1.6%; Score 17, DB Best Local Similarity 100.0%; Pred. No. 47, Matches 17; Conservative 0; Mismatches
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Patent No. 577671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 100.0%; Pi
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                  439 AAAATCCCGACGACGAC 455
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TELBFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 748 base pairs
                                                              LENGTH: 516 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 748 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA HYPOTHETICAL: NO ANTI-SENOT
                                                                                                                                         linear
                                                                                                                                                                                                        ANTI-SENSE: NO
IS-08-510-878-2
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Sequence 6792, Application US/09252991A

Sequence 6792, Application US/09252991A

Sequence 6792, Application US/09252991A

Sequence 6792, Application US/09252991A

Setent No. 651791

Trie OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PREUDOMONAS

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PREUGINGA FOR DIAGNOSTICS AND THERAPEUTICS

TITLE OF INVENTION: 107196,136

CURRENT APPLICATION NUMBER: US/09/252,991A

CURRENT FILING DATE: 1999-02-18

PRIOR APPLICATION NUMBER: US 60/074,768

PRIOR APPLICATION NUMBER: US 60/094,190

PRIOR FILING DATE: 1998-07-27

NUMBER OF SEQ ID NOS: 33142

LENGTH: 882
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLERC ALID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS:
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO GST8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ö
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TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 867;
47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 17; DB 4; Length 882;
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ATTORNEY/AGENT INFORMATION
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                       Query Match
Best Local Similarity 100.0
Matches 17, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO.
SEQUENCE CHARACTERISTICS
                                     nucleic acid
                                                                                 linear
                                                          STRANDEDNESS:
TOPOLOGY: lin
                                                                                                  , MOLECULE TYPE:
US-09-195-940-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              US-09-562-466-1
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APPLICANT: Grossman, Alex
APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Amgen Canada Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2; Length 1353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0; Indels
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APPLICATION NUMBER: US/09/195,940
                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
CITY: Mississauga
STATE: Ontario
COUNTY: Canada
ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Pelence.
                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.6%; Score 17;
                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
                                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/611,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/09195940 Patent No. 6258935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 100.0%; P
Matches 17; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        622 GIGGCICAGCAACTICT 638
                                                                                                                                                                                                                                                                                                                                                                                        34,688
                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION VUMBER: 34,68
REFERENCE/DOCKET NUMBER: A
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1353 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                      Floppy disk
                                                                                                           STATE: Ontario
COUNTY: Canada
ZIP: LSN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: CDNA
                                                                                      Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-195-940-1/c
                                                                                                                                                                                                                                                 SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-611-280-1
                                                                                        CITY: N
STATE:
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Gaps
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Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSE: American Canada Inc.
STREET: 673 Mississauga Road, Suite 303
CITY: Mississauga
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Oncario
COUNTRY: Canada
ZIP: LEN 6JB
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                Length 1353
                                                            Indels
                DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/DOCKET NUMBER: A-338A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/195,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: CDNA SEQUENCE DESCRIPTION: SEQUENCE DESCRIPTION: SEQUENCE
                                                                                                                                                                                                                                                                                                                                         APPLICANT: Matsuyama, Toshifumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-09-553-867A-42/c
; Sequence 42, Application US/09553867A
; Patent No. 6476188
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 01-May-2000
CLASSIFICATION: <Unknown>
1.6%; Score 100.0%; Pre
                                                                                                                                                                                                                                                                   Sequence 1, Application US/09562466 Patent No. 6369202 GENERAL INFORMATION:
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APPLICANT: Grossman, Alex
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING LSIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 17; DB 2; Length 12537;
                                                                                                                                                                                                                                                                                                                                                         DB 3; Length 3758;
45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3: Amgen Canada Inc.
6733 Mississauga Road, Suite 303
                                                                                                                                                                                                                                                                                                                                                      Query Match 1.6%; Score 17; DB Best Local Similarity 100.0%; Pred. No. 45; Matches 17; Conservative 0; Mismatches
                                                                                                                   PRAGMENT TYPE: N-terminal ORIGINAL SOURCE: ORGANISM: Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 4, Application US/08611280
Patent No. 5891666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            8349 Grégorcaccacarcir 8333
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IBM PC compatible
SYSTEM: PC-DOS/MS
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ATTOREY/AGRET INFORMATION:
NAME: Oleski, Nancy A.
REGISTRATION NUMBER: 34,688
REFERENCE/POCKET NUMBER: A.
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                     linear
E: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 12537 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP. LSN GJB
COMPUTER READABLE FORM:
MEDIUM TYPE: Flor-
COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Mississauga STATE: Ontario
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC
OPERATING SYSTEM:
SOFTWARE: Patenti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 17; Conserva
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                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
LOCATION:
US-08-323-477-1
                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US-08-611-280-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Sparling, P. Frederick
APPLICANT: Thompson, Stuart
TITLE OF INVENTION: N. MENINGITIDIS RELATED TO THE HEMOLYSIN PAMILY OF TOXINS
TOWNERS OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Imclone Systems Incorporated
                                                                           APPLICANT: Price, Jeffrey
APPLICANT: Takahashi, Joseph S.
APPLICANT: Philip, Lowey L.
TILE OF INVENTION: A NOWEY L.
TILE OF INVENTION: A NOWEY L.
CURRENT APPLICATION NUMBER: US (99/553, 867A
CURRENT APPLICATION NUMBER: 60/090, 068
PRIOR APPLICATION NUMBER: 60/090, 068
PRIOR FILING DATE: 1998-06-18
PRIOR FILING DATE: 1998-06-18
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 42
LENGTH: 1960
                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Primer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.6%; Score 17; DB 4; Length 1960;
100.0%; Pred. No. 46;
tive 0; Mismatches 0; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/323,477
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEE: Imclone Systems Incorporated
1: 180 Varick Street
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/920,963
FILING DATE: 28-UUL-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: United States of Americ
ZIP: 10014
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          equence 1, Application US/08323477 aatent No. 6086896 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                761 CCGCCGCCGCTGCTTCG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101 ccecceccecrecrice 85
                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 1.6
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Feit, Irving N. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S-09-553-867A-42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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GENERAL INFORMATION:
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Matsuyama, Toshifumi
APPLICANT: Grandson, A.A.
APPLICANT: Richardson, Christopher D.
TITLE OF INVENTION: NOVEL GENES ENCODING ISIRF POLYPEPTIDES
TITLE OF INVENTION: NOVEL GENES ENCODING ISIRF POLYPEPTIDES
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Canada Inc.
STREET: 673 Mississauga Road, Suite 303
CITY: Mississauga Road, Suite 303
CITY: Canada
STRATE: Ontario
COUNTRY: Canada
ZIP: LSN 636
COMPUTER REAPABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: DatentIn Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/09/195,940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 1.6%; Score 17; DB 3; Length 12537; Best Local Similarity 100.0%; Pred. No. 44; Matches 17; Conservative 0; Mismatches 0; Indels (
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Patent No. 6258935
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Search completed: February 2, 2004, 07:58:50 Job time : 89.3221 secs

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Ltd.		h time 801.301 Seconds alignments) Million cell updates/sec	.cacggtcatcgaaccactga 1071				4869878			COMB. seq: *  PUB. seq: *  PUB. seq: *  COMB. seq: *  COMB. seq: *  COMB. seq: *  COMB. seq: *  COMB. seq: *  BCOMB. seq: *  FUB. seq:	iComB. seq: ∗	chance to have a result being printed, istribution.	<i>:</i>	Description	
GenCore version 5.1.6 (c) 1993 - 2004 Compugen	using sw model	, 03:00:32 ; Searcl {without 4871.226	:	Gapext 60.0	822278265 residues		chosen parameters:	00	45 summaries	ublished Applications NA:*  / cgn2	data/1/pubpna/US60_PUB	results predicted by to the score of the of the total score d	SUMMARIES	ID	US-09-938-842A-1034 US-09-938-842A-1034 US-09-770-444-615 US-09-770-444-615 US-09-770-696-257 US-10-295-3770-4 US-10-269-403-147 US-10-269-403-170-4 US-10-245-603A-1 US-10-245-603A-1 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316 US-09-918-995-30316
Ge Copyright (c)	eic search,	February 2, 2004	US-09-938-842A-1034 1071 1 atggcgacaattcagaagct	OLIGO NUC Gapop 60.0 , Ga	2434939 segs, 18	0	hits satisfying	ength: 0 ength: 20000000	: Listing first	Published Appl: 11. / cgn2	co.	o. is the number of rester than or equal lerived by analysis o	de	Query Match Length DB	0.000 000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.000 0.
	M nucleic - nucl	no on:	itle: erfect score: equence:	coring table:	earched:	ord size :	otal number of	inimum DB seq l aximum DB seq l	ost-processing:	atabase		Pred. No. score grea and is der		esult No. Score	00000 00000

Sequence 5485, Ap	Sequence 64, Appl	Seguence 216038.	Sequence 216038,	Sequence 739, App	4	4	Sequence 337, App	r	Sequence 27151, A	Sequence	Sequence 57, Appl	Sequence	Sequence 1, Appli	Sequence 1, Appli	Sequence 787, App	Sequence 5500, Ap	Sequence 370, App	Sequence 370, App	Sequence 1265, Ap	Sequence 273, App	Sequence 1982, Ap	Sequence 328, App	Sequence 675, App	Sequence 116, App	Sequence 323443,	Sequence 324847,	Sequence 323443,	324847,	6933,	TO STATE	
1.7 432 10 U	1.7 475 9 US-	1.7 572 13 US	1.7 572 14 US	1.7 626 9∷US∓	1.7 1119 12 US	1.7 1487 12 US	18 1.7 2577 10 US-09-938-842A-337	1.7 2577 12 US	1.7 3086 12 US	1.7 3757 12 US	1.7 4721 12 US	1.7 14353 13 US	1.7 162450 13 US	1.7 162450 15 US	1.6 344 9 US-	1.6 385 10 US	1.6 396 10 US	1.6 396 12 US	1.6 402 10 US	1.6 406 10 US	1.6 435 11 US	1.6 442 15 US	1.6 490 11 US	1.6 498 9 US-	1.6 543 13 US	1.6 543 13 US	1.6 543 14 US	1.6 543 14 US	563 10 US		ALIGNMENTS
c 16	-	-	c 19	N	21	22	c 23	N	25	~	~	0 28	N	30	c 31	m	m	m	m	.c 36	M	38	39	40	4	4,	4	4,	c 45		

Sequence 1034, Application US/0938842A

Sequence 1034, Application US/0938842A

Sequence 1034, Application US/0938842A

GENERAL INFORMATION:
APPLICANT: Kreps, Joel
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: APPLICANT: NAME, AND METHODS OF DIANTS, TRANSGENIC PLANTS CONTAINING
ITILE OF INVENTION: SAME, AND METHODS OF USE
ITILE OF INVENTION: SAME, AND METHODS OF USE
ITILE OF INVENTION: SAME, AND METHODS OF USE
CURRENT APPLICATION NUMBER: US/09/938,842A

CURRENT FILING DATE: 2001-08-24

PRIOR APPLICATION NUMBER: US/60/264,647

PRIOR PILING DATE: 2001-01-16

PRIOR PILING DATE: 2001-01-16

PRIOR FILING DATE: 2001-06-22

NUMBER OF SEQ ID NOS: 5379

SEQ. ID NO 1034

LENGTH: 1071 TYPE: DNA Property ORGANISM: Arabidopsis thaliana Property US-09-938-842A-1034

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Query Match 100.0%; Score 1071; DB 10; Length 1071; Best Local Similarity 100.0%; Pred. No. 0; Matches 1071; Conservative 0; Mismatches 0; Indels 0; Gaps

APPLICANT: Wang, Xun
APPLICANT: Zhu, Tong
APPLICANT: Zhu, Tong
TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSCENIC PLANTS CONTAINING
TITLE OF INVENTION: SAME AND METHODS OF USB
TITLE OF INVENTION: SCRIPLIOG-3
CURRENT FILING DATE: 2001-08-24
PRIOR PPLICATION NUMBER: US 60/227, 866
PRIOR FILING DATE: 2000-08-24
PRIOR FILING DATE: 2001-01-16
PRIOR PLILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
PRIOR PLILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/300,111
NUMBER OF SEQ ID NOS: 5379
SEQ ID NO 1034
LENGTH: 1071

121 CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTTCAATGTCTTTTA 180 121 CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTTTTTCAATGTCTTTA 180	181 GCTCCACCGTCTTCGACAGGACCACCATGAAGAGAGTTCGACTAAAAGACCGTCACACG 240 181 GCTCCACCGTCACCACCACCACCACCAACAAAAAAAAAA	A AGGTTGAAGGAAGAGAAAGATACGAATACCTGCCACGTGCGGGTTGCCTGCC	241 AAGGTTGAAGGAAGAAGGAAGGATACGGATGCCTGCCACGTGTGCGGCTGGGATTTTT 300	301 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGGCGAAACGATTCGGTGGTTGTTGGAG-360-361 CAATTAACTCGAGAGTTAGGTCACAAATCCGACGACGAAACGATTGGTGTTGGAG-360-361 CAATTAACTCGAGAGTTAAGGTCACAAATCCGACGAAACGATTCGGTGGTTGTTGGAG-360-360-361 CAATTAACTCGAAAGATTAACTAAATCCGACGAAACGATTCGGTGGTTGTTGGAG-360-360-360-360-360-360-360-360-360-360	361 AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATCGCCATG 420	361 AACGCTGAGCCGGCGATTATAGCCGCCACGGGTACGGGAACGGTTCCCGCCATGGCATG 420	421 TCGGTTAACGGAACCTTAAAAATCCCGACGACGACGACGATGTTCTGATATGGGTGAA 480 421 TCGGTTAACGGAACCTTAAAAATCTCGACGACGACGACGACGACGACGACGACGACGACGACGAC	81 AATCTGATGAAGAAACGTAAACGACCTTCTAAACAAGTATATATA	1 AATCTGATGAAGAAGAAGAAGTAAACGACCTTCTAACAGTGAGTATATAGACATAAGCGAC	541 GCCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACCAAGGATCCAACCTCCG 600	_	601 CAAGCICIGGCAICCAICCACIGIGGCICAGCAACIICIGCGCAAGGAAIGTAICGGAIG. 660	601 CAAGCTCTGGCATCATCCACTGTGGCTCAGCAACTTCTGCCGCAAGGAATGTATCCGATG 660	661 TGGGCTATTCCATCAAACGCAATGGTTCCGACGGCGGGGGCGTTCTTCTTCTTCATTCCACAA 720		721 ATCGCTGGTCGGATCAGCTCAGTTATTAGCTTTTCCGCCGCGCGCTGCTTCGCCG 780	721 ATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTCGCCG 780	TCGTCTTACGTCGCCGCTGTTCAACAGCTTCCACGATGGCTAGACCACCTCCTTTACAA 84	ol lusicitads concerned and a	011	1 のこのかのはアスカーコンのこのできない。 これをおける アンド・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・アン・	GCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACAACCGGTATATCATCGTCA	961 ATTGCAACAACGACGCACGCACACGCTGAGACACTTCATTCA	61 ATTGCAACAACAACGACGCGACACGCTGAAGAACTTCTCCCTAGAGATATACGAAAACAA 102	1021 GAGCTTCACCAGTTCATGAGCACCACAACGACGACCACTGA 1071	1021 GAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCATCGAACCACTGA 1071	1000   1000
oy Gb	<u>ک</u> ج	ò	Ob	Oy Db	٥٪	qq	y d	ò	op Q	δ,	QQ	λ	qc	237	ପ୍ପ	č	qo		3 8	දු දු	8 8	. a	Š	: 음	Š	qa	

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               541 GCGTTTCAGCTTCCTCCGGTTTAGCTCCAATTGCCACGACGACGACGATCCAACCTCCG 600
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                                                                                                                                          1 ATGGCGACAATTCAGAAGCTTGAAGAAGTTGCAGGCAAAGATCAAACTCTAAGAGCCGTT
                                                                                                                                                                                 1 AIGGCGACAAITCAGAAGCITGAAGAAGTIGCAGGCAAAGATCAAAACTCIAAGAGCCGIT
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                                                                                                                                                                                                                                                                                                          121 CCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGGTGATGCCGTCGTTTTCAATGTCTTTA
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                                                                                                         Gaps
                                                                DB 12; Length 1071;
                                                                                                       :
                                                                                                         Indels
                                                                                                     ;0
                                                              Query Match 100.0%; Score 1071; Best Local Similarity 100.0%; Pred. No. 0. Matches 1071; Conservative 0; Mismatches
, ORGANISM: Arabidopsis thaliana
US-09-938-842A-1034
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RESULT 2

S.09-038-042A-1034
Sequence 1034, Application US/09938842A
Publication No. US20040009476A9
GENERAL INFORMATION:
APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel

OY 900 AGCGACGTCGGTTATGGCTCCGAGCTCAGGCGTAACAACCGGTAGTTCATCGTC 959	-770-444-615/ uence 615, App ent No. UGS200 ERAL INFORMATI PLICANT: An, PLICANT: An, PLICANT: PTI PLICANT: PTI		OF INVENTION: EFERNCE: 202 TAPPLICATION T. FILING DATE APPLICATION IN C. FILING DATE: OF SEQ ID NO RB: FaetSEQ fi H: 453	<pre>/; TYPE: DNA // ORGANISM: Arabidopsis thaliana // FEATURE: // TWANS/KEY: misc feature // LOCATION: (1) (453) // OTHER INFORMATION: n = A,T,C or G US-09-770-444-615</pre>	Query Match   26.7%; Score 286; DB 9; Length 453; Best Local Similarity   100.0%; Pred. No. 3.9e-145;     Best Local Similarity   100.0%; Pred. No. 3.9e-145;     Matches 286; Conservative   0; Mismatches   0; Indels   0; Gaps   0;     Oy
	vaacaa 	ESULT 3 S-09-224-035A-502/C Squence 502, Application US/09924035A Patent No. US20020142319A1 GENERAL INFORMATION: APPLICANT: Grlach, Jrn TITLE OF INVENTION: Expressed Sequences of Arabidopsis FILE REFERENCE: 201US CURRENT APPLICATION NUMBER: US/09/924,035A CURRENT FILING DATE: 2000-08-11 PRIOR APPLICATION NUMBER: US 60/148,784 PRIOR FILING DATE: 1999-08-13 NUMBER OF SEQ ID NOS: 900	SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 5.02 LENGTH: 460 TYPE: DNA TYPE: DNA READINE: FEATURE: FEATURE: LOCATION: (1)(460) OTHER INFORMATION: n = A,T,C or G	Ouery Match  Best Local Similarity 99.6%; Pred. No. 9.1e-147;  Matches 459; Conservative 0; Mismatches 1; Indels 1; Gaps 1;  \$600 GCAAGCTCTGGCATGTGCACTGTGGCTCAGCAAGGAATGTATCGAT 659  460 GCAAGCTCTGGCATCATGTGTATCTACTAATCTAATCAAATGTATCTAATAATAATAATAATAATAATAATAATAATAATAA	60 GIGGGCTATTCCATCAAACGCAATGATTCCGACGGAGCTTTCTTCTTGATTCCACA 400 GIGGGCTATTCCATCAAACGCAATGATTCCGACGGAGCTTTCTTCTTGATTCCACA 400 GIGGGCTATTCCATCAAACGCAATGATTCCGACGGAGCTTTCTTCTTGATTCCACA 720 AATCGCTGGTCCGACGATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCTGCTTCGCC 740 AATCGCTGGTCCGTCGAATCAGCCTCAGTTATTAGCTTTTCCCGCCGCCGCCGCTGCTTCGCC 780 GTCGTCTTACGTCGCCGCTGTTCAACAGGCTTCCACACACA

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61 AAACTICAAGACCTITCCAAGTAATCCCACAGTGAGTCTCGAGCCCAAGGCGGAGCCGG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95 AAACTICAAGACCTTTCCAAGTAAATCCCACAGTGAGTCTCGAGGCCAAGGCGGAGCCGG 154
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106 TCGTCAATTGCAACAACAACGACGCGCACACGCTGAGAGACTTCTCCCTAGAGATATATACGAG 47
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                                                                                  1015 AAACAAGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1060
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                                                                                                                                      46 AAACAAGAGCTTCACCAGTTCATGAGCACCACAACAGCACGGTCAT 1
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17.3%; Score 185; DB 9; Length 18
Best Local Similarity 100.0%; Pred. No. 4.9e-90;
Matches 185; Conservative 0; Mismatches 0; Indels
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APPLICANT: Davis, Keith R.
APPLICANT: Allen, Keith A
APPLICANT: Allen, Keith
APPLICANT: Hoffman, Neil
APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: LAMIana
FILE REFERENCE: 2031US (PARA-020PRV)
CURRENT APPLICATION NUMBER: US/09/770,696
CURRENT APPLICATION NUMBER: 60/178,278
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQ ID NOS: 911
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                             se 257, Application US/09770696
No. US20010044940A1
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Publication No. US20030101481A1
GENERAL INFORMATION:
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US-09-770-696-257
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atthew, Abraham V
edford, Brooke L.
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Hamilton, Carol M.
Price, Jennifer L.
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ameaka, Joshua G.
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Gaps
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APPLICANT: Hinkle, Gregory J.
APPLICANT: Start, Steven C.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Goldman, Barry S.
APPLICANT: Chen, Xianfeng
TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN
TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
FILE REFERENCE: 38-10(52052) B/
CURRENT APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR APPLICATION NUMBER: US 60/360,039
PRIOR PILING DATE: 2002-02-28
NUMBER OF SEQ ID NOS: 47374
SEQ ID NO 37704
LENGTH: 1263
                                                                                                                                                                                                                                                                                   FILE REFERENCE: MEI-0003
CURRENT APPLICATION: PLANT GENE SEQUENCES I FILE REFERENCE: MEI-0003
CURRENT APPLICATION NUMBER: US/10/295,403
CURRENT FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: US/09/394,519
PRIOR FILING DATE: 1999-09-13
PRIOR APPLICATION NUMBER: 60/101,349
PRIOR FILING DATE: 1998-09-22
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR APPLICATION NUMBER: 60/103,312
PRIOR FILING DATE: 1998-11-17
PRIOR FILING DATE: 1998-11-22
NUMBER OF SEQ ID NOS: 170
SOFTWARE: PATENTEN IN VET: 2.0
SOFTWARE: PATENTEN VET: 2.0
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2.1%; Score 23; DB
Best Local Similarity 100.0%; Pred. No. 0.1
Matches 23; Conservative 0; Mismatches
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Publication No. US20030233675A1
GENERAL INFORMATION:
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; ORGANISM: Pseudomonas fluorescens
US-10-369-493-37704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: DNA
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                   Benito, Maria-Ines
Yu, Guo-Liang
Fromm, Mike
rd, Jacqueline
echmann, Jose
                                                                                                                                                                      eddie, James
hang, James
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; LOCATION: (143)..(1345)
; OTHER INFORMATION: G802
US-10-295-403-147
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Best Local Similarity
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Gaps

Indels

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Length 34094;

DB 16; 20;

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APPLICANT: Lalgudi, Raghunath, V.
APPLICANT: Ito, Laura, Y.
APPLICANT: Sherman, Bradley, K.
TITLE OF INVENTION: POLYVICLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN TASSEL PILE REFERENCE: PL-0009 US
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) OTHER INFORMATION: Incyte ID No. US20010051335A1 700354854H1

) NAME/KEY: unsure

) LOCATION: 96, 99-100, 198, 205

) OTHER INFORMATION: a, t, c, g, or other

US-09-294-093B-4716
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100.0%; Pred. No. 62;
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1.8%; Score 19; DB
Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches
                           CURRENT FILING DATE: 2002-12-10
PRIOR APPLICATION NUMBER: US 09/292,034
PRIOR APPLICATION NUMBER: US 60/081,882
PRIOR FILING DATE: 1999-04-14
PRIOR FILING DATE: 1998-04-15
NUMBER OF SEQ ID NOS: 8
SOFTWARE: FRECEEQ for Windows Version 3.0
LENGTH: 34094
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/294,093B
CURRENT FILING DATE: 1999-04-16
PRIOR APPLICATION NUMBER: 60/082,567
PRIOR FILING DATE: April 21, 1998
NUMBER OF SEQ ID NOS: 6207
SQFTWARE: PERL PROGRAM
SEQ ID NO 416
LENGTH: 277
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PRIOR APPLICATION NUMBER: US/09/235,076
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Publication No. US20030073623A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                              TYPE: DNA ORGANISM: Porcine Adenovirus Type 3
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US-09-294-093B-4716/c
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     0; Indels
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CURRENT APPLICATION NUMBER: US/10/199,550
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: US 09/963,038
PRIOR FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: TIKOO, Suresh Kumar
APPLICANT: BABIUK, Lorne A.
TITLE OF INVENTION: PORCINE ADENOVIRUS TYPE 3 GENOME
FILE REFERENCE: 293102002410
                                                                                                                                                                                                          Sequence 1, Application US/09963038A
Publication No. US20030143200A1
GENERAL INFORMATION:
APPLICANT: Tikoo, Suresh K.
TITLE OF INVENTION: PORCINE ADENOVIRUS E1 REGION
FILE REPRENCE: 293102003200
CURRENT APPLICATION NUMBER: US/09/963,038A
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 18
SOFTWARE: FRESERG for Windows Version 4.0
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100.0%; Pred. No. 200.
0; Mismatches
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches
  0; Mismatches
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ORGANISM: Porcine Adenovirus Type 3
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APPLICANT: REDDY, Police Seshidhar APPLICANT: TIKOO, Suresh Kumar
                                             764 CCGCCGCTGCTTCGCCGTCG 783
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LENGTH: 34094
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Matches
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Gaps
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TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REPERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DAIE: 2001-07-30
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Length 277;

FILING DATE: 1999-01-20

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0; Gaps
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Publication No. US20030073623A1
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
FILE REFERENCE: 20411-756
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: PRESEQ for Windows Version 3.0
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63;
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63;
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APPLICANT: AJGATE, Paul A.
APPLICANT: MAINION, JOHNSON BELLOANT: MAINION, JOHNSON BELLOANT: MAINION, COMPOSITIONS AND METHODS FOR THE TETILE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER.
FILE REPERENCE: 210121.493
CURRENT APPLICATION NUMBER: US/09/777,564
CURRENT FILING DATE: 2001-02-05
NUMBER OF SEQ ID NOS: 1730
SOCIETARE: FastSEQ for Mindow Version 4.0
SEQ ID NO 1604
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SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 30316
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atent No. US20020591A1
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, OTHER INFORMATION: n = A,T,C or G
US-09-918-995-30316
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Matches 18; Conservative 0;
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Best Local Similarity 100.(
Matches 18; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                         NAME/KEY: misc_feature
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CORGANISM: Homo sapiens
US-09-918-995-34549
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CRGANISM: Homo sapiens
US-09-777-564-1604
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LENGTH: 377
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.493C1
CURRENT PAPPLICATION NUMBER: US/10/015,219
CURRENT FILING DATE: 2002-03-02
NUMBER OF SEQ ID NOS: 1739
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1604
LENGTH: 424
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Mismatches 0; Indels
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Publication No. US20030008299A1
GENERAL INFORMATION:
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Best Local Similarity 100.0%; Pi
Matches 18; Conservative 0;
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CRGANISM: Homo sapiens
US-10-015-219-1604
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Bukaryota, Viridiplanteas, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

(bases 1 to 91884)
Lin, X., Kaul,S., Town,C.D., Benito,M.-I., Creasy,T.H., Haas,B.J.,
Wu,D., Maiti,R., Ronning,C.M., Koo,H., Fujii,C.Y., Utterback,T.R.,
Barnstead,M.E., Bowman,C.L., White,O., Nierman,W.C. and Fraser,C.M.
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2 BAC F17K2 genomic_sequence,
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1621 GCTTTTAACAACTCTCGTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTTA 1677
                                                                                       AAAGGACGGACGATAGGAGGATTTTGGAATCCTGGAAAGAGGATTATTCCATAGACACTA
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              ATTAGCTTTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCCCAAGTATG
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                                                                 AAAAGAAAACATTTTGTGAAAAGAGAAATAAAGTTTACTGGACCCCATTGTACAGATGG
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AC003680
AC003680.3 GI:20197048
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AC003680/c
LOCUS
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KEYWORDS
SOURCE
ORGANISM
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Patent: WO 0216655-A 3729 28-FEB-2002;
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AESQKDTFKRILKIDLSFPLTPNVSEEAKNLISQLLVKDFSKRLSIEKIMQHPWIVKN
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ESQATFRIVASASLTSKANIDSIMSTRSTSBNRARSRLKASET LGFOGTVSNPDDLVII
ESQATNKPOSLDDAVLRRLVKRIYVPLPDSNVRKLLFRTKLKCQFHSLSDGDIDKIVKT
TEGKLYRLCIKKRRPISQVTDKRYSGSDLQALCEEAAMPIRELGANILITIQANKVLN
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IRDVTFSHEKTTDVNGFVESINEEALDEMHYLHAALSETIRLYPPVPVDMRCAENDDV
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/gene="At2g45520"
/note="Synonym: F17K2.5; supported by full length cDNA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="#yroonym: F17K2.3; predicted by genscan"
complement (join(<3414. .3616,3639. .3825,3916. .3965,
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db.xref="G1:2979543"

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gene="At2g45510"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://ccr.001.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant http://www.igt.org/softlab/glimmerm.html, and GeneSplicer (Mihaela Pertea, mprediction cagainst a peptide database and the plant EST database at TIGR mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by ERNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE) inclinis. Genes encoding tRNAs are predicted by http://ftp.genome.washington.edu/RM/Repeatmasker (Arian Smit, http://tp.genome.washington.edu/RM/Repeatmasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oin(57. 242,335. 747)
gene="At2g45480"
note="Protein sequence is in conflict with the conceptual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /trānslation="DESKPSVQKFFPEVSDKCLBAAKPSSNRKNDIIARSREWKNNVV
KOGLPHGIPRESPTYLQERGCFRLQVPTDNBEPGCRRTDGKKRRCSKDVLSGQKYCD
KHWIRCRNKKKHPVDTTNSHBNAGFSFLTVETAVRSVVPCKDGDDQKHSVSWMGITLPR
VSDEKSTSSCSTDTTITDTALRGEDDDESYLSLFSPGV"
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/note="overlap with BAC clone F4L23 (AC002387:1. .1281)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(1002, .2388)
/gene="Ar2g45450"
/note="synonym: F17K2.2; contains a protein kinase domain
profile (PDGC00100)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BAC clone F17K2 is from Arabidopsis thaliana chromosome 2 and is near the molecular marker(s) FLS.

The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                           Direct Submission
Submitted (09-MAR-2000) The Institute for Genomic Research, 9712
Medical Center Dr., Rockville, MD 20850, USA
3 (bases 1 to 91854)
                                                                                                                                                                                                                                                                                                                                                                                                                   9712
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1655. .1750,1886. .2128,2260. .>2388))
                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (27-FBB-2002) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtown@tigr.org On Apr 18, 2002 this sequence version replaced gi:6598396. Address all correspondence to:at@tigr.org
Arabidopsis thaliana chromosome 2 BAC F17K2 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/cultivar="Columbia"
/db xref="taxon:3702"
/db zref="taxon:40"
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yroduct="hypothetical protein"
protein_id="AAF18607.2"
db_xref="GI:20197053"
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Submitted (27-FEB-2002) The Institute
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join(<57. .242,335. ,>747)
gene="At2g45480"
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                                                                                    (bases 1 to 91854)
                                                                                                                                                                                                                                                                                                                      'own, C.D. and Kaul, S.
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CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACGTTACCTCG
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        CCTCTGTGGGGCCCGAATCTGTAATCGGAAAAGGTGGAACCCACTTGGTTTAACTTTT
                                                                                                                       AAGCCTAAAAGGTTACTTACTGGTTTTATAATTTTGGTGTTTAATTCTAATCCC
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                                                                                                                                                                                          GGATCCGTTTGTTTAATCTCAAGGCCACGTTATCGCCAATATTTGATTTTTGAGTG
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Complement (join(<10833. 11272,11438. .11560/11636/ 12378,

12454. 12937,13023. .13119,13284. 13374,13464. .13548,

13455. 13794,13957. .144073,14478. .14264,14350,114418,

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15568. .16244,16322. .16465,16545. .17093,17237. .17431/,

17612. .17696,18015. .18613,18844. .19249,19533. .19714,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /trānslation="MQSSSSGGDDLEKQQQQQKDKSPQKQSESANESNHLTIVVCN
GDSSRELVGQIPPEKEVSLSRNGSSHEQCRVCLQDKEVLIBLGCQCGKGGLAKHRS
GIDAMPRIKGSNQCEICQVVA,NVTPPPETQPTTNYWWRIDPSYRQERERGGFSPLM
VAFSILLGGLMLDVLISITLGVSALPVNIIIGVIVVLGLGTALRLTLEFCYEWSLRRA
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Pred. No. 0;
; Mismatches
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complement(10833. .25573)
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                                                                                                                                                            9408 .9427 (CA)n"
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complement (9578 .9632)
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9822 .10798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      btein_id="AAC06154.1"
xref="G1:2979545"
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9948. .10670
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Bricaryota, Viridiplantae; Streptophyta, Embryophyta, Tracheophyta;

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1 (bases 1 to 1660)

Yamada, K., Liu, S.X., Sakano, H., Pham, P.K., Banh, J., Chung, M.K.,

Goldsmith, A.D., Lee, J.M., Quadh, H.L., Toriumi, M., Yu, G., Bowser, L.,

Carninci, P., Chen, H., Cheuk, R., Hayashizaki, Y., Ishida, J.,

Jones, T., Kamiya, A., Karlin-Neumann, G., Kawai, J., Kim, C., Lam, B.,

Lin, J., Miranda, M., Narusaka, M., Nguyen, M., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Shinozaki, K.,

Arabidopsis Full Length cDNA Clones

Arabidopsis Full Length cDNA Clones

RS Yamada, K., Banhi, J., Tang, C.C., Toriumi, M., Yamamura, Y.,

Yu, G., Yu, S., Bowser, L., Carninci, P., Chen, H., Cheuk, R.,

Hayashizaki, Y., Ishida, J., Jones, T., Kamiya, A., Karlin-Neumann, G.,

Kawai, J., Kim, C., Koesema, E., Lam, B., Lin, J., Mayers M. C.,

Miranda, M., Narusaka, M., Nguyen, W., Palm, C.J., Sakurai, T.,

Satou, M., Seki, M., Shinn, P., Southwick, A., Tracy, S. B.,

Shinozaki, K., Davis, R.W., Ecker, J. R. and Theologis, A.

Birect Submission

AL Submitted (12-SEP-2001) Plant Gene Expression Center, 800 Buchanan Street, Albany, C.A. 94710, USA

RIKEN Genomic Sciences Center (GSC) members carried out the

Collection and clustering of Rafl cDNAs (Rawi, J.), Kawai, J.,

Kawaidopsis Pull-Length CDNA, Saki, M., Narusaka, M., Ishida, J.,

Satou, M., Kamiya, A., Sakurai, Y.
         1286 TITITIAGAICATCAAGGCICCIACAGAITICITAGGGAAIGGITICAGGCTITIGITA 1345
                                                                                                                                                                                                                      1406 TAAGCTTCTCTATGTCTAAGAAATGGACCGATAGGAATAAAACAACATCATTAAAGAT 1465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY056214 1660 bp mRNA linear PLN 18-SEP-2002
Arabidopsis thaliana putative PCF2 DNA binding protein (At2g45680)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Annotation is based on the January 2002 version of the Arabidopsis genome submitted to GenBank.

Location/Qualifiers

1. 1660
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                                                                                                                     1346 GARATTGTGTTTTTTGCARCAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA
                                                                  121 GAAATTGTGTTTATTGCAACAGGTAGAAACATAAACCATAGACAGATGTATCTGAAGAGA
                                                                                                                                                                              181 TAAGCTTCTCTATGTCTAAAGAAATGGACGATACGAATAAAACAAGCATCATTAAAGAT
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28)
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AY056214
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Arabidopsis thaliana shrunken seed protein (SSE1) mRNA, complete
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AFKGIFTINEAMKYNTRALFRENSOTWOLLGGGETPNBEKDSNGSEQNRAGNSGRN
LGPHGLGNONHHNPWNLEGRAMSALSSFGQNARTITSSTPGWSRRIGHQQAVIEPPMI
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KKLELIPLIGFLTEKIVELLEGAQSRYTYISGS"
268 c 347 g 407 t
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
Lin, Y., Sun, L., Wguyen, L.V., Rachubinski, R.A. and Goodman, H.M. The Pexi6p homolog SSEI and storage organelle formation in Arabidopsis seeds
Science 284 (5412), 328-330 (1999)
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                                                                                                                                                                  Din.Y., Sun,L., Nguyen,L.V. and Goodman,H.M.

Lin,Y., Sun,L., Nguyen,L.V. and Goodman,H.M.

Submitsion

Submitted (19-AUG-1998) Molecular Biology, Massachusetts General

Hospital, 50 Blossom Street, Boston, MA 02114, USA
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11.5%; Score 193; DB 8; Length 1483;
Best Local Similarity 99.6%; Pred. No. 3.7e-95;
Matches 243; Conservative 0; Mismatches 1; Indels
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mol type="mRNA"
culfivar="C24"
db xref="taxon:3702"
chromosome="2"
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AF085354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACCESSION
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2

RIGIN

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TITLE
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AUTHORS
TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TREIGHKSDGETIRWILENAEPAIIAATGTGTVPAIAWSVNGTIKIPTTTVADSDMGE
NLMKKKRKRPSNSEYIDISDAVSASSGLAPIATTTTIQPPQALASSTVAQQILPQGNY
PMWAIPSNAMIPTVGAFFLIPQIAGPSNQPQILLAFPAAAASPSSYVAAVQQASTWARP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1576 CTTGGACGTGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCT 1635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ALLUBZUU 250957 bp DNA linear HTG 13-MAY-2003
Rattus norvegicus clone CH230-20C16, *** SEQUENCING IN PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   translation="MATIQKLEEVAGKDQTLRAVDLTIINGVRNVETSRPFQVNPTVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PPLOVVPSSGFVSVSDVSGSNLSRATSVMAPSSSSGVTTGSSSSIATTTTHTLRDFSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JEPKAEPVMPSFSMSLAPPSSTGPPLKRASTKDRHTKVEGRGRRIRMPATCAAR
                                                                                                             'clone="RAFL07-08-P04 (R10678)"
'note="This clone is in a modified pBluescript vector
(FLC-1) as a BamHI/KhoI insert.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 product="putative PCF2 DNA binding protein"
protein_id="AAL07063.1"
'db_xref="GI:15810351"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1660;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 dercercarcaccarcarrincicicaectarrina 102
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AC106200.4 GI:30579164
HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
Rattus norvegicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6.1%; Score 102; DB 8; L llarity 100.0%; Pred. No. 1.4e-44; Conservative 0; Mismatches 0;
organism="Arabidopsis thaliana"
mol_type="mRNA"
db_xref="taxon:3702"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           411 t
                                                                                                                                                                                                                                                                                                                                                                                                                         evidence=experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     385 g
                                                                                                                                                                                                  ecotype: Columbia"
                                                                                                                                                                                                                    .1660
gene="At2g45680"
                                                                                                                                                                                                                                                                               . .102
gene="At2g45680"
                                                                                                                                                                                                                                                                                                                                                                 gene="At2g45680"
codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="At2g45680"
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Best Local Simil
Matches 102; (
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AC106200/c
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KEYWORDS
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ORIGIN.
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Gunarathe, P. Haaland, W., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Hamilton, C., Howells, S., Hlalyk, S., Hume, J., Idhebird, D., Jackson, A., Gackson, A., Hogel, S., Halyk, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., Kelly, S., London, P., Longarre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longarre, S., Lopez, J., Liu, J., Liu, Y., London, P., Longarre, S., Lopez, J., Mangua, D., Martin, K., Martin, K., Martin, K., Martin, K., Martin, S., Martinez, E., Mangua, P., Martin, K., Martin, K., Martin, S., Martin, S., Martin, S., Martin, S., Martin, S., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, M., Markin, 
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On May 13, 2003 this sequence version replaced gl:23118058.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (http://www.hgsc.bcm.tmc.edu/projects/rat/). Each conting described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffout'). Within each contig-acaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both and sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table.
Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W.,
Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (12-JAN-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor Collège of Medicine, One Baylor Plaza, Houston, TX 77030, USA

3. (bases 1 to 250557)

Rat Genome Sequencing Consortium.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-heip@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Center project name: GJUV
Center clone name: CH230-20C16
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AUTHORS
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AUTHORS
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JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     282156 bp DNA linear HTG 19-NOV-2002
Rattus norvegicus clone CH230-291E4, *** SEQUENCING IN PROGRESS
24719-3-1
                                                                                           NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bom.tmc.edu/docs/Genbank_draft_data.html)
NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently consists of 3 contigs. The true order of the pieces is not known and thair order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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Consensus quality: 238092 bases at least Q20
Estimated insert size: 250301, sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia; Eutheria, Rodentia, Sciurognathi, Muridae, Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
1.4%; Score 24; DB 2; Length 250957;
Best Local Similarity 100.0%; Pred. No. 0.3;
Matches 24; Conservative 0; Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                          1 247058: contig of 247058 bp in length 247058: gap of unknown length 24828: contig of 1070 bp in length 248328: gap of unknown length 250957: contig of 2629 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a 490\overline{8}1 c 49937 g 74548 t 11052 others
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HTG: HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
Rattus norvegicus (Norway rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       organism="Rattus norvegicus"
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complement(243703. .244577)
//note="cloue_boundary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="wgs_end_extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="wgs_end_extension
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mol_type="genomic DNA"
db_xref="taxon:10116"
clone="CH230-20C16"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1097 CATAAAATTAAAGTAAATCTTTTT 1120
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245116. .247058
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note="clone_boundary"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 clone_end:Sp6
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248229
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EFINITION
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C119331
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Bryant, N., Bulay, C., Hurchl, F., Burrell, K., Cadesor, E.,
Cardens, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.
Chacko, J., Chaver, D., Chen, G., Chen, P., Chen, D.,
Claveland, C., Cockrell, R., Cax, C., Coyle, M., Cree, A., D'Souza, L.
Claveland, C., Davy-Carroll, L., Dand, R., Dinh, H., Divya, K.,
Dagado, Denson, S., Derna, A., Durbin, K., Duval, B., Baves, K.,
Brandez, S., Finley, M., Flagg, N., Forbes, L., Fenle, T., Fan, G.,
Fraser, C.M., Gabisi, A., Garta, R., Garcia, A., Garner, M., Gebergordis, E., Geer, X., Gill, R., Garcia, A., Garner, M., Gebergeorgis, E., Geer, X., Gill, R., Gracia, A., Garner, M., Gebergeorgis, E., Geer, X., Gill, R., Gracia, M., Garcia, M., Garcia, M., Gebergeorgis, E., Geer, X., Gill, R., Grady, M., Garcia, M., Gebergeorgis, E., Georgia, M., Hamilton, C., Hamilton, C., Hamilton, K., Harnandez, J., Havlak, P., Hladun, S. L., Hodgeon, M., Hernandez, J., Harlys, R., Hulyk, S., Hume, J., Idebird, D., Jacksen, A., Jacksen, L., Eddson, A., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Johnson, R., Jacksen, J., Jacksen, J., Labow, H., Levan, J., Lawis, M., Marine, S., Huly, S., Kelly, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Khan, Z., King, L., Kovar, C., Kovis, C., Kraft, C.L., Loulseged, H., Lozdon, R., Martinez, E., Mandhart, M., Mantadartne, M., Manner, G., Milles, M., Martinez, E., Martinez, E., Mandhart, M., Morris, S., Mulleson, M., Morris, S., Mulleson, M., Morris, S., Mulleson, M., Morris, S., Mulleson, M., Mulleson, M., Mulleson, M., Morris, C., Newly, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Kally, S., Mulleson, M., Morris, C., Manja, P., Martinez, E., Mulleson, M., Morris, C., Martinez, E., Mulleson, M., Morris, C., Martinez, C., Serelle, R., Savery, G., Scherer, S., Scott, G., Sale, M., Savery, G., Scherer, S., Scott, G., Sale, M., Savery, G., Scherer, S., Scott, G., Sale, R., Kally, S., Kally, S., Kally, S., Kal Submitted (19-NOV-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

On Nov 19, 2002 this sequence version replaced gi:23911491.

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads; assembled using Atlas (http://www.hgsc.bm.tmc.edu/projects/raft/). Each contig described in the feature table below represents; a scaffold in the Atlas ssembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and ordered and separated by sized gaps filled with Ns to the Setimated, and separated by sized gaps filled with Ns to the Setimated say be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence reads. Both end sequences and whole genome table. Submitted (26-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA (bases 1 to 282156)
Rat Genome Sequencing Consortium. Burch, P., Burrell, K., Calderon, E., 2 (bases 1 to 282156) Worley, K.C. Direct Submission Unpublished

Center: Baylor College of Medicine

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Gaps

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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                           Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;
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Patent: WO 0128540+A 30 26-APR-2001;
                                                                                                                                  Therapy of cephalic pain
Patent: WO 0128540-A 29 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Sequence 30 from Patent W00128540:
AX114618
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Seguence 29 from Patent WO0128539:
AX114743
                                                                                                                                                                                                                                    organism="Homo sapiens"
                                                                                                                                                                                                                                                        /mol_type="genomic_DNA".
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/db_xref="taxon:9606"
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Location/Qualiflers
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                      Homo sapiens (human)
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                                          Homo sapiens
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AX114618/c
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NOTE: This sequence may represent more than one clone.
NOTE: This is a "working draft' sequence. It currently
consists of 5 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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                                                  Center project Information
Center project name: CH230-291E4
Center clone name: CH230-291E4
Assembly program: Phrap; version 0.990329
Consensus quality: 253046 bases at least Q40
Consensus quality: 255012 bases at least Q30
Consensus quality: 255010 bases at least Q30
Consensus quality: 255010 bases at least Q30
Consensus guality: 25460; sum-of-contigs estimation
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation
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clone_end:Sp6"
86729 a 49533 c 48244 g 75688 t 21962 others
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                                  Contact: hgsc-help@bcm.tmc.edu
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Sequence 29 from Patent WO0128540.
AX114617
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /mol_type="genomic DNA"
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75<u>9</u>79. .277096
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/note="clone_boundary
clone_end:T7
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complement[209107.
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Best Local Similarity 100.0
Matches 24; Conservative
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277197
278295
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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1.4%; Score 23; DB 6; Length 101;
Best Local Similarity 100.0%; Pred. No. 1.3;
Matches 23; Conservative 0; Mismatches 0; Indels
                                                                           DB 6; Length 101;
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Diagnostic test for cephalic pain
Patent: WO 012925-A 29 26-APR-2001,
GLAXO GROUP LIMITED (GB)
LOCATION/Qualifiers
                                                                         Query Match
Best Local Similarity 100.0%; Pred. No. 1.3
Matches 23; Conservative 0; Mismatches
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Cephalic pain susceptibility marker
Patent: WO 012926-A 28 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Sequence 29 from Patent WO0129255.
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/mol_type="genomic DNA"
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/db_xref="taxon:9606"
          /db_xref="taxon:9606"
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AX118673.1 GI:14035624
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Matches 23
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Butel
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Agent for treating cephalic pain
Patent: WO 0128539-A 29 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Agent for treating cephalic pain
Patent: WO 0128539-A 30 26-APR-2001;
GLAXO GROUP LIMITED (GB)
LOCATION/Qualifiers
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Diagnostic test for cephalic pain
Patent: WO 0129255-A 28 26-APR-2001,
GLAXO GROUP LIMITED (GB)
LOCATION/QUALIFIERS
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Matches 23; Conservative
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Search completed: February Job time : 6370.7 secs

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Test for the diagnosis of diabetes and compounds for the treatment
thereof
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Homo sapiens
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Cephalic pain susceptibility marker
Patent: WO 0129356-A 29 26-APR-2001;
GLAXO GROUP LIMITED (GB)
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Best Local Similarity 100.0%; Pred. No. 1.3
Matches 23; Conservative 0; Mismatches
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Sequence 28 from Patent W00233121.
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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Identifying a stress condition to which a plant cell has been exposed and producing plants with increased tolerance to these abiotic stresses.

Claim 144; SEQ ID NO 3729; 577pp + Sequence Listing; English

invention relates to identifying a stress condition to which a plant. It has been exposed, comprising:

contacting nucleic acid representative of expressed polynucleotides the plant cell with an array or probes representative of the plant

Cell genome; and the state of expressed polynuclectures in the plant cell genome; and profile of expressed polynuclectures in the plant cell production of transgence presents. The method is useful in the plants production of transgence plants, cells and seeds and in producting plants with increased tolerance to abiotic stress. The present sequence is that of an Arabidopsis thalians stress regulated gene (ABZ12196-ABZ17574) used in methods of the invention.

Note: The sequence data for this patent is not represented in the printed specification but is based on sequence information supplied to Derwent by the European Patent Office.

Sequence 1677 BP; 508 A; 292 C; 335 G; 542 T; 0 other;

0; Gaps DB 24; Length 1677; 0; Indels ; Score 1677; D; Pred. No. 0; 0; Mismatches 100.0%; Query Match Best Local Similarity 100. Matches 1677; Conservative à

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TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT 1465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATIGIGITITATIGCAACAGGIAGAGAACATAACCATAGACAGAIGTATCIGAAGAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel shrunken seed gene useful for producing transgenic plants having altered production of food storage reserve material, intracellular transport of storage protein and formation of protein or oil bodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTTAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAAATTGTGTTTATTGCAACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TAAGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TTTTTCAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is that of Arabidopsis thaliana SSE1 (shrunken seed) cDNA, which was isolated from a seedling cDNA library using a partial genomic clone as probe. SSE1 encodes a protein (see AAB19718) that, when expressed in a cell of a plant, modifies or alters the production of a food storage reserve material (e.g. protein, lipid or carbohydrate storage reserve), facilitates the intracellular transport of a storage protein, or facilitates the formation of protein or oil bodies. The invention provides a transgenic plant (or plant cell, plant tissue, plant organ or plant component) which includes a recombinant SSE1 transgene that modifies the production of food storage reserves, thereby
                                                                       storage reserve; storage protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1483 BP; 461 A; 268 C; 347 G; 407 T; 0 other;
                                                                                                                                                                                                                                Location/Qualifiers
122..1225
/*tag= a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 57; 64pp; English
Arabidopsis thaliana SSE1 cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 increasing nutritional value.
                                                                SSE1; shrunken seed gene; st
oil body; transgenic plant;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 11.5%;
Best Local Similarity 99.6%;
Matches 243; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-APR-2000; 2000WO-US09192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              99US-0128651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (GEHO ) GEN HOSPITAL CORP
                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-679483/66
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                                                                                                                                                                                                                                                                                                                                                                       WO200061735-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1226
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Lin Y;
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directly or indirectly the insulin receptor or insulin receptor signalling pathway in the manufacture of a medicament for preventing or treating cephalic pain. Also described is an isolated polymorbecide (II) or protein (III) comprising a polymorphism that causes susceptibility to cephalic pain, or a naturally occurring polymorphism that is in linkage disequilibrium with the first polymorphism (I) has antimigraine and vulnerary activities. (I) is useful for treating cephalic pain which may be a cluster headache, chronic paroxysmal hemicrania, headache associated with vascular disorders, headache associated with substances or their withdrawal (for example drug withdrawal), tension headache and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ly or indirectly insuling receptor or
in the manufacture of medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention describes the use of an agent (I) that modulates
                                                                                                                                                                                 SNP; migraine; cephalic pain; insulin receptor signalling pathway; antimigraine; vulnerary; cluster headache; chronic paroxysmal hemicra vascular disorder associated headache; withdrawal; tension headache;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            represents an insulin receptor oligonucleotide containing a migraine associated polymorphic site, which is used in the exemplification of
                                                                                                                                                                   Insulin receptor; polymorphic site; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                                                          /*tag= a
/standard_name= "single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1.4%; Score 23; DB 22; Length 101; 00.0%; Pred: No. 0.69;
                                                                                                                                   Insulin receptor migraine associated polymorphic site #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in particular migraine with or without aura. The represents an insulin receptor oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  insulin receptor signaling pathway ir
preventing or treating cephalic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Use of agent that modulates directly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               223 ACAAGCATCATTAAAGATTAAAT 245
                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               53
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                                                                                                                                                                                                                                                                                                        replace (51,A)
                                AAH50475 standard; DNA; 101
                                                                                                                                                                                                                                                                                                                                                                                                                                            19-OCT-2000; 2000WO-GB04031.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99GB-0024713.
                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Purvis IJ, McCarthy LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FI; 2001-300274/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                          WO200128539-A2
                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19-OCT-1999;
                                                                                               21-AUG-2001
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Best Local Si
Matches 23
                                                              AAH50475;
                                                                                                                                                                                                                                                                                                        allele
RESULT 3
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RESULT 4

1345

120

9

Gaps

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Score 193; DB 21; Length 1483; Pred. No. 5.9e-85; 0; Mismatches 1; Indels 0

An antisense construct is useful for

1405

migraine; ds. Homo sapiens.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Diagnosis of susceptibility to migraine in individuals comprises the identification of polymorphisms in the insulin receptor gene region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; insulin receptor; antimigraine; cephalic pain; diagnosis; susceptibility; single nucleotide polymorphism; SNP; SNP detection;
                                                                                                                                                                                                                                                                                             Human; insulin receptor; diagnosis; cephalic pain; susceptibility; single nucleotide polymorphism; SNP; migraine; SNP detection; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
replace(51,A)
/*tag= a
/standard_name= "Single nucleotide polymorphism"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human insulin receptor gene polymorphic site INSBa.
                                                                                                                                                                                                                             Human insulin receptor gene polymorphic site INSBa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (SNP) in the human insulin receptor gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH31269 standard; DNA; 101 BP.
                            AAH31172 standard; DNA; 101 BP.
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                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Purvis IJ, McCarthy LC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLAX ) GLAXO GROUP LTD.
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                                                                                                                                                              25-JUL-2001
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
variation
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                                                                                               AAH31172;
AAH31172/c
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AAH31269/c
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The present sequence is provided in a specification relating to a method for diagnosing susceptibility to cephalic pain in an individual. The method comprises typing in vivo or in a sample from the individual, the insulin receptor gene region or insulin receptor individual, the insulin receptor gene region or insulin receptor cause susceptibility to cephalic pain have been found. Susceptible to cause susceptibility to cephalic pain have been found. Susceptibility may be diagnosed using a probe, primer or antibody which is capable of detecting an insulin receptor gene region or insulin receptor protein polymorphism. The method is useful for diagnosing susceptibility to migraine, cluster headache, chronic paroxysmal hemicrania, headache associated with vascular disorders, headache associated with substances or their withdrawal, tendion headache, and so on. It is useful for assessing the efficacy of agents in relieving cephalic pain, and can be used to assess the ability of agents to modulate insulin and can be used to assess the education and/or susceptibility of an individual to the development of new drug therapies which selectively target one or more allelic variants of the insulin receptor and in the allelic variants of the insulin receptor and in the allelic variants of the insulin receptor and in the prelent parameter of the present sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Diagnosing susceptibility to cephalic pain such as migraine by typing insulin receptor gene or protein in vivo, or in a biological sample and determining individual's susceptibility to cephalic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               corresponds to a polymorphic site and flanking sequences of a sin
nucleotide polymorphism (SNP) in the human insulin receptor gene
                                                                                                                  /*tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 23; DB 22; Length 101; Pred. No. 80.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INSBa polymorphism of human insulin receptor gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
1.4%; Score 23; DB
Best Local Similarity 100:0%; Pred. No.*0.6
Matches 23; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    223 ACAAGCATCATTAAAGATTAAAT 245
                                                                        Location/Qualifiers replace (51, A)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75 ACAAGCATCATTAAAGATTAAAT 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example; Page 21; 46pp; English.
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                                                                                                                                                                                                                                                                                                                                                                               Purvis IJ, McCarthy LC;
                                                                                                                                                                                                                                                                                                                                       (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-316247/33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    corresponds to
                                                                                                                                                                              WO200129256-A2
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                                                                              Key
variation
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Homo sapiens.

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The present invention relates to the use of an agent that modulates directly or indirectly the insulin receptor or insulin receptor signalling pathway in the manufacture of a medicament for preventing or treating cephalic pain. Cephalic pain disorders are generally multifunctional disorder, with a cluster of headache, chronic paroxysmal hemicrania, headache associated with vascular disorders, paroxysmal hemicrania, headache and in particular migraine with aura or migraine without aura. The treatment of cephalic pain and migraine or migraine without aura. The treatment of cephalic pain and migraine pathways, in particular by manipulation of the glucose and lipid metabolism pathways, in particular by manipulation of the insulin receptor. Insulin receptor is an important component in the regulation of the glucose and lipid metabolism pathways. Single nucleotide polymorphisms (SIP) in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of agent that modulates directly or indirectly insulin receptor insulin receptor signaling pathway in manufacture of medicament for preventing or treating cephalic pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ulin receptor ĝene contribute to susceptibility to cephalic pain.
present sequence is INSBa polymorphism of human insulin receptor
Human; insulin receptor; cephalic pain; therapy; headache; chronic paroxysmal hemicrania; vascular disorder; tension headache; migraine; single nucleotide polymorphism; SNP; ds.
                                                                                                                                                                                                                                                                                      /standard_name= "Single nucleotide polymorphism"
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Pred. No. 0.69;
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                                                                                                                                                                                            Location/Qualifiers
replace (51, A)
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ABQ72727 standard; DNA; 101
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ses 23; Conservative
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19-OCT-1999;
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                                                                                                                                  Homo sapiens
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variation
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SNP; migraine; cephalic pain; insulin receptor signalling pathway; antimigraine; vulnerary; cluster headache; chronic paroxysmal hemicrania; vascular disorder associated headache; withdrawal; tension headache; ds.
                                                                                                                                                                                                                                                                                                                                                                             he invention relates to a novel method for diagnosing diabetes or susceptibility to diabetes in an individual. The method of the invention has antidiabetic activity. The method is useful for diagnosing diabetes or susceptibility to diabetes in an individual. Other methods of the invention are is useful for treating diabetes and for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence contains a single nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polymorphic site; single nucleotide polymorphism;
                                                                                                                                                                                                                                                                                         Diagnosing diabetes or susceptibility to diabetes in individual by typing insulin receptor gene region or insulin receptor protein in sample obtained from individual
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Insulin receptor gene exons 14-17 including introns SEQ ID NO:25.
                                                     *tag= a
/standard_name= "Single nucleotide polymorphism"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  polymorphism (SNP) present in the human insulin receptor gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 23, DB 24; Length 101;
Pred. No. 0.69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 101 BP; 26 A; 15 C; 14 G; 46 T; 0 other;
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100.0%; Pred. No. ...
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                          Location/Qualifiers
replace (51,A)
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ID AAHSOS70 standard; DNA; 7240 BP.
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99US-0160423.
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                                                                                                                                                                                                          (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                       Hosford D, Purvis IJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insulin receptor;
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                                         variation
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25-JUL-2001 (first entry)
Purvis IJ, McCarthy LC;
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The present invention describes the use of an agent (I) that modulates directly or indirectly the insulin receptor or insulin receptor treathed is an edicament for preventing signalling pathway in the manufacture of a medicament for preventing treating cephalic pain. Also described is an isolated polymochotide (II) or a naturally occurring polymorphism that causes susceptibility to ephalic pain, or a naturally occurring polymorphism that is in linkage disequilibrium with the first polymorphism. (I) has antimigraine and be a cluster headache. Chronic paroxysmal hemicrania, headache associated with vascular disorders, headache associated with substances or their withdrawal (for example drug withdrawal), tension headache and in particular migraine with or without aura. The present sequence represents exons 14-17 from the insulin receptor gene including introns, which is used in the exemplification of the present invention.
                                                                                                  Use of agent that modulates directly or indirectly insulin receptor or insulin receptor signaling pathway in the manufacture of medicament for preventing or treating cephalic pain
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                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 54-57; 58pp; English.
WPI; 2001-300274/31.
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1.4%; Score 23; DB 22; Length 7240; 100.0%; Pred. No. 0.56; tive 0; Mismatches 0; Indels 0 Ouery Match
Best Local Similarity 100..
These 23, Conservative

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AAH31170 standard; DNA; 7240 BP AH31170/c

AAH31170;

Human insulin receptor gene, exons 14 to 17.

Human; insulin receptor; diagnosis; cephalic pain; susceptibility; single nucleotide polymorphism; SNP; migraine; SNP detection; ds.

Homo sapiens

WO200129255-A2

26-APR-2001.

19-OCT-2000; 2000WO-GB04024

99GB-0024717

19-OCT-1999;

(GLAX ) GLAXO GROUP LTD

Purvis IJ, McCarthy LC;

WPI; 2001-328499/34

Diagnosis of susceptibility to migraine in individuals comprises the identification of polymorphisms in the insulin receptor gene region

Disclosure, Page 38-41; 41pp; English

The present sequence is provided in a specification relating to a method of diagnosing susceptibility to cephalic pain. Polymorphisms

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The present sequence is provided in a specification relating to a method for diagnosing susceptibility to cephalic pain in an individual. The method comprises typing in vivo or in a sample from the comparises typing in vivo or in a sample from the comparises typing in vivo or insulin receptor individual, the insulin receptor gene region or insulin receptor contains that is susceptible to caphalic pain. Polymorphisms in the insulin receptor gene that caphalic pain. Polymorphisms in the insulin receptor gene that any be diagnosed using a probe, primer or antibody which is capable of detecting an insulin receptor gene region or insulin receptor protein polymorphism. The method is useful for diagnosing susceptibility to migraine, cluster headache, chronic paroxysmal hemicrania, headache associated with vascular disorders, headache associated with substances or their withdrawal, tension headache, and so on. It is useful for assessing the efficacy of agents in relieving cephalic pain, and can be used to assess the ability of agents to modulate insulin receptor signalling activity. The method may also be used to assess correction and/or susceptibility of an individual to the development of diseases mediated by the insulin receptor and in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing susceptibility to cephalic pain such as migraine by typing insulin receptor gene or protein in vivo, or in a biological sample and determining individual's susceptibility to cephalic pain
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              cephalic pain, particularly to migraine. The method comprises typing a region of the insulin receptor gene or insulin receptor protein of an individual. A susceptibility to cephalic pain may be diagnosed using a probe, primer or antibody which is capable of detecting a polymorphism in an insulin receptor gene region or the insulin receptor protein.
in the insulin receptor gene have been found to cause susceptibility
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, insulin receptor; antimigraine; cephalic pain; diagnosis;
susceptibility; single nucleotide polymorphism; SNP; SNP detection;
migraine; ds.
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Pred. No. 0.56;
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100.0%; Pred. No. v...
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                                                                                                                                                                                                                                           23; Conservative
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AAH31267/c
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Pred. No. 0.5 Mismatches

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Local Similarity

Query Match

23;

Best Loca Matches

5056 ACAAGCATCATTAAAGATTAAAT 5034

AAD04467 standard; DNA; 7240

SULT 11

223 ACAAGCATCATTAAAGATTAAAT 245

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he invention relates to a novel method for diagnosing diabetes or susceptibility to diabetes in an individual. The method of the invention has antidiabetic activity. The method is useful for diagnosing diabetes or susceptibility to diabetes in an individual: other methods of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for treating diabetes and for treating and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             typing insulin receptor gene region or insulin receptor protein sample obtained from individual
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention are is useful for treating diabetes and for tre
preventing diabetes. The present sequence represents the
      Indels
                                                                                                                                                                                                                                                                                                                                                   Human; insulin; receptor; diabetes; antidiabetic; ds
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    Mismatches
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                                                                                  5056 ACAAGCATCATTAAAGATTAAAT 5034
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                                           223 ACAAGCATCATTAAAGATTAAAT 245
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100.0%; Pre-
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                                                                                                                                                                                                                                                                                                            Human insulin receptor gene
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      Conservative
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    23;
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    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insulin receptor gene contribute to susceptibility to cephalic pain. The present sequence is complete sequence from exon 14 to 17 of human insulin receptor gene. SNP in this sequence contributes to susceptibility
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to the use of an agent that modulates directly or indirectly the insulin receptor or insulin receptor of signalling pathway in the manufacture of a medicament for preventing or treating pathway in Cephalic pain disorders are generally multifunctional disorder, with a cluster of headache, chronic paroxysmal hemicrania, headache associated with vascular disorders, headache associated with substances or their withdrawal (for example drug withdrawal), tension headache and in particular migraine with aura or migraine without aura. The treatment of cephalic pain and migraine pathways, in particular by manipulation of the insulin receptor. Insulin receptor is an important component in the regulation of the glucose and lipid metabolism pathways. Single nucleotide polymorphisms (SNP) in the
development of new drug therapies which selectively target one or more allelic variants of the insulin receptor gene.
                                                                                                                                               Gaps
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in manufacture of medicament for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; insulin receptor; cephalic pain; therapy; headache;
chronic paroxysmal hemicrania; vascular disorder; tension headache;
migraine; single nucleotide polymorphism; SNP; ds.
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                                                                                                    Score 23; DB 22; Length 7240;
Pred. No. 0.56;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7240 BP; 1952 A; 1653 C; 1820 G; 1815 T; 0 other;
                                                            Sequence 7240 BP; 1952 A; 1653 C; 1820 G; 1815 T; 0 other;
                                                                                                                                               0; Indels
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Human insulin receptor DNA (from exons 14 to 17).

04-JUL-2001

AAD04467;

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Gaps

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Disclosure, Page 42-45; 46pp; English.

Use of agent that modulates directly insulin receptor signaling pathway in preventing or treating cephalic pain

99GB-0024712.

Purvis IJ, McCarthy LC; WPI; 2001-290815/30

(GLAX ) GLAXO 19-0CT-1999; 19-0CT-1999;

19-OCT-2000; 2000WO-GB04051

WO200128540-A2

26-APR-2001

Homo sapiens.

autoimmune disorder; inflammation; angiogenic diseases; AIDS; acquired immunodeficiency syndrome; hepatitis; anaemia; wound healing;

DB 22; Length 7240; 0.56;

1.4%; Score 23; 100.0%; Pred. No.

Query Match Best Local Similarity

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ABZ73281-ABZ73697 represent cDNAs corresponding to 391 human secreted protein genes, and ABP00947-ABP01363 represent the proteins they encode. ABZ73698-ABZ73698 represent human secreted protein genemic fragments. The invention also encompasses antibodies specific for the secreted proteins in drug screening and recombinant the use of the secreted proteins in drug screening and recombinant covectors and host cells comprising a nucleic acid of the invention. The secreted proteins are thought to be involved in biological activities associated with cellular signalling, cellular differentiation, cell screening and neurotransmitter activity. The secreted proteins, nucleic acids encoding them, antibodies or antibody fragments specific for the secreted proteins, and encoding them, antibodies or antibody fragments specific for the secreted proteins and modulators of proteins activity are useful for diagnosing or treating cancers or other hyperproliferative disorders. Additionally, the secreted proteins and their nucleic acids may also be used in the treatment of autoimmune disorders, inflammatory disorders, diseases involving angiogenesis, ADS (acquired immunodeficiency syndrome), hepathtis, anaemia, and to promote wound healing. Nucleic acids of the invention may be used for chromosome definition and the secreted proteins and the secreted immunodeficiency syndromes in the invention and to promote the secreted proteins and the secreted immunodeficiency syndromes, the secreted promote the secreted proteins and the secreted immunodeficiency syndromes, the secreted promote the secreted secreted syndromes and the secreted syndromes and the secreted syndromes and the secreted syndromes and the secreted syndromes and the secreted syndromes and the secreted syndromes and the secreted syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes and syndromes 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New human secreted proteins and nucleic acids, useful for detecting or treating cancer or other hyperproliferative disorders, autoimmune disorders, inflammatory disorders, HIV disease, hepatitis or anemia -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein genomic fragment referred to in the disclosure of the
drug screening; chromosome identification; chromosome mapping; cytostatic; gene therapy; antiinflammatory; immunomodulator; anti-HIV; antianaemic; vulnerary; gene; ds.
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ABT17023 standard; DNA; 17646 BP.
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12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                               WO200277013-A2
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Human; secreted protein; nootropic; neuroprotective; cytostatic; anti-HIV; virucide; dermatological; immunosuppressive; antiinfilamatory; anti-HIV; vulneray; antibacterial; antiparkinsonian; antisickling; antianaemic; antiarthritic; cancer; antiparkinsonian; hepatotropic; cerebroprotective; antialtarthritilammatory; antiallergic; antidabetic; antilucer; anticonvulsant; antifungal; antiparastic; cardiant; immuno disorder; infection; vaccine; cardiovascular disorder; neurological disease; nephrotropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention comprises the amino acid and coding sequences of human secreted proteins. The DNA and protein sequences of the invention are useful for the diagnosis and treatment of allergic disorders, asthmatic disorders and immediate hypersensitivity diseases (e.g. hay fever, allergic conjunctivities and allergic rhinitis). The proteins of the invention are also useful for identifying a binding partner. The nucleic acids of the invention are also useful for chromosome identification, radiation hybrid mapping or long-range restriction mapping. The present DNA sequence.
allergic disorder; asthmatic disorder; gene therapy; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Use of human secreted proteins and nucleic acids for preparing a diagnostic or pharmaceutical composition for diagnosing or treating allergic or asthmatic disorders, e.g. asthma, hay fever, or allergic
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100.0%; Pred. No. 1.7;
ive 0; Mismatches 0; Indels 0
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                          hay fever; allergic conjunctivitis; allergic rhinitis;
binding partner identification; chromosome identification;
radiation hybrid mapping; long-range restriction mapping.
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12-SEP-2001; 2001US-0950082.
12-SEP-2001; 2001US-0950083.
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1es 22; Conservative
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27-MAR-2001, 2001US-278650P.
12-SEP-2001, 2001US-0950082.
12-SEP-2001, 2001US-0950083.
                                           26-MAR-2002; 2002WO-US09188
03-OCT-2002
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(HUMA-) HUMAN GENOME SCI INC. Rosen CA, Ruben SM; WPI,, 2003-040583/03.

New human secreted proteins encoded by genes contained in cDNA clones (e.g. HGCAC19), useful for preventing, treating or diagnosing e.g. ALDS, multiple sclerosis, herpes virus, leukemia, tick-borne encephalitis or west Nile fever

Disclosure; Page 2326-2330; 2423pp; English.

The invention relates to novel human genes (ABZ66891-ABZ68209) and the encoded secreted proteins (ABP99470-ABP99872) useful for preventing, treatment ameliocating medical conditions e.g. by protein or gene therapy. The genes are isolated from a range of human tissues disclosed in the specification. The nucleic acids, proteins, antibodies and (anti-agonists are useful in the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and ovarian cancer and other and cuter of the adrenal gland, bone, bone marrow, breast, gastrointestinal tract, liver, lung or unceprential; (b) immune discorders e.g. Addison's disease, allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid architis and ulcerative colitis; (c) cardiovascular disorders such as myocardial ischaemias; (d) wound healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f) infectious diseases such as viral, bacterial, fungal and parasitic infections.

Sequence 17646 BP; 5370 A; 3099 C; 3561 G; 5616 T; 0 other;

Gaps ö Length 17646; 0; Indels Query Match
1.3%; Score 22; DB 25;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 22; Conservative 0; Mismatches 0;

1133 TAAAAATTATTGAAAATCTTTC 1154 

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Search completed: February 2, 2004, 03:13:29
Job time : 496.761 secs

8.9 278 8.9 347 6.0 486 5.1 378	4.9 146 28 BH617024	1.6 825 28 BH493162 1.3 207 29 AL764163 1.3 162 28 AQ055392 1.3 178 10 BE933474	1.3 258 10 BF703799 1.3 269 14 CB477075 1.3 310 9 AA224031 1.3 318 9 AW480642	1.3 329 9 AW358594 1.3 330 9 AA224071 1.3 349 14 CD470137	1.3 365 9 AI466455 1.3 391 14 CA940873	1.3 406 10 BF449231 1.3 413 10 BE207343	1.3 424 9 AIO35951 1.3 440 10 BF707341	1.3 445 9 AU18421 1.3 455 9 AU1844421	1.3 476 10 BF707342 1.3 488 13 BX281427	1.3 521 10 BF704377 1.3 551 9 AW655154	1.3 555 10 BF284594 1.3 564 12 BM384056 1.3 587 12 PT527137	1.3 599 10 BG539984 1.3 639 10 BG539984	1.3 637 10 BE254600 1.3 663 28 B53012	1.3 702 14 CB309574	1.3 711 10 BE251436 1.3 728 10 BB610568		ALIGNMENTS		O C C	nsertion lines 45:45:x, genomic		562927.1 GI:28177691 S.		Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta; Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, rosids	eurosids 11; brassicates; brassicaceae; Arabidobsis. (bases 1 to 317) pnso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab Jacke & Karnea M. Kim C. J. Darker H., Prednia L., Shinn P.	ion Mutations in the	abidopsis Genome published	ntact: Joseph R. Ecker 1k Institute Genomic Analysis Laboratory (SIGnAL)	The Salk Institute for Biològical Studies 110010 N. Torrey Pines Road, La Jolla, CA 92037, USA Tel: 858 453 4100 x1752 Fax: 858 558 6379
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GenCore version 5.1 Copyright (c) 1993 - 2004 Con	M nucleic - nucleic search, using sw model	00:53:06	utle: US-09-938-842A-3729 Perfect score: 1677 Jequence: 1 ggttaagcgttttacttatg	<pre>icoring table: OLIGO NUC</pre>	earched: 22781392 segs, 12152238056 resid	ford size : 0	otal number of hits satisfying chosen parameter	iinimum DB seq length: 0 Aximum DB seq length: 200000000	ost-processing: Listing first 45 summaries	latabase : BST:*	1: em_estba:* 2: em_estbum:* 3: em_estin:*	4: em_ester: *	6: em_estpl:* 7: em_estro:*	8: em_htc:* 9: qb_est1:*	10: <u>gb_est2:*</u> 11: qb_htc:*	12: gb_est3:* 13: db_est4:*	14: gb_est5:* 15: em_estfun:*	16: em_estom:* 17: em_gss_him:*	18: em_uss_inv:	20: em gas Vrt.: 21: em gas fun:*		24: em_gss_pro:* 25: em_gss_rod:*	26: em_gss_phg:* 27: em_gss_vrl:*	28: gb_gssl:* 29: gb_gss2:*	Pred. No. is the number of results predict score greater than or equal to the score and is derived by analysis of the total sc		\$ Query	Score Match Length DB	1 271 16.2 317 29 BZ662927 2 245 14.6 267 29 AL761108 3 164 9.8 232 28 BH612074 4 164 9.8 233 28 BH612075

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/clone="SALK 02642.45.x"
/clone="SALK 02642.45.x"
/clone="BALK 02642.45.x"
/note="PCR was performed on Arabidopsia thaliana lines
/note="PCR was performed on Arabidopsia thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"

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                                This is single pass sequence recovered from the left border of IDNA. This sequence lies within 300 bases of the 5' end of
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/strain="Columbia 0"
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Email: ecker@salk.edu
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Eukaryofa; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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flanking the insertion. Sequences displaying significant
similarity to the A. Inlaina muclear genome sequence were
processed for submission. T-DNA derived sequences were
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                                              Direct Submission
Submitted (17-UIN-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (17-UIN-2002) Weisshaar B., Max-Planck-Institut fuer
Zuechtungsforschung, Carl-von-Linne-Weft border of the T-DNa. It
This sequence is recovered from the left border of the T-DNa. It
Indicates an insertion within the locus defined by clone f44:8. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koelin.mpg.de/GABI-Kat/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                569
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    (bases 1 to 232)
    Alonso, J. M., Leisse, T. J., Barajas, P., Chen, H., Cheuk, R., Gadrinab, C., Useke, A., Kalonso, M., Kim, C. J., Parker, H., Prednis, L., Shinn, P., Zimmerman, J. and Ecker, J. R.

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/clone lib="Arabidopsis thaliana T-DNA insertion lines"
/note="PCR was performed on DNA from Arabidopsis thaliana
plants (T1) which were transformed with the T-DNA from
vector PACI61. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
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Rosso, M., Li, Y., Strizhov, N. and Weisshaar, B.
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/organism="Arabidopsis thaliana"
/--> '''n=""aenomic DNA"
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Pred. No. 3.2e-113;
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Arabidopsis thaliana
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/strain="Columbia_0"
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Best Local Similarity 100.0%
Matches 245; Conservative
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B2377781 GSS 26-NOV-2002
SALK 106185.39.30.x Arabidopsis thaliana TDNA insertion lines
Arabidopsis thaliana genomic clone SALK_106185.39.30.x, genomic
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Spermatophyta, Pagmollophyta, eudicotyledons, core eudicots, rosids
servesids II, Brassicales, Brassicaceae, Arabidopsis
1 (bases 1 to 278)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         183 AGCTICTCTATGTCTAAAGAAATGGACCGATACGAATAAAACAAGCATCATTAAAGATTA 242
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                                                                                                                                                                                                                                                  /db_xxef="taxmn:3702"
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/clone="SALK_032104"
/clone="lb="Arabidopsis thaliana TDNA insertion lines"
/clone="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used cabe found at http://signal.salk.edu/tdna_protocols.html*
a 45 c 47 g 83 t salk.edu/tdna_protocols.html*
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A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
                                128 AATGGTTTGTAAGAAATACTACACTTATTTATGTGAAATTGTGTGGGTTAGTGAAAAGTAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9:8%; Score 164; DB 28; Length 233; 100:0%; Pred: No: 6:3e-72;
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Salk Institute Genomic Analysis Laboratory (SIGnAL)
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10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
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Fax: 858 558 678 679
Email: ecker@salk.edu
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                                                                                                                                                                         organism="Arabidopsis thaliana"
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/organism="Arabidopsis thallana"
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/strain="Columbia 0"
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           ecker@salk.edu
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1 (bases 1 to 233)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., "Geke,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimmerman,J. and Bcker,J.R.
Arabidopsis Genome
Unpublished
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="caxon:3702"
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/clone lib="Arabidopsis thaliana lines and rote="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion elements. The resultant fragment for each line was directly sequenced to determine the genomic sequence at the site of insertion. Details of the protocols used can be found at http://signal.salk.edu/tdna_protocols.html"

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                                                                         Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGnAL)
The Salk Institute for Biological Studies
10010 N. Torrey Panes Road, La Jolla, CA 92037, USA
Tel: 858 453 4100 x1752
Fax: 858 558 6379
Email: ecker@salk.edu
This is single pass sequence recovered from the left border of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 AGCTTCTCTATGTCTAAAGAAATGGACCGATACGAATAAAAACAAGCATCATTAAAGATTA
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  of Insertion Mutations in the
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Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
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Tel: 858 453 4100 x1752
Fax: 858 558 6379
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                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/mol type="genomic DNA"
/strain="Columbia 0"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9.8%; Score 164; DB 28;
100.0%; Pred. No. 6.3e-72;
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Arabidopsis thaliana
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Sequence-Indexed Library
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                             Arabidopsis Genome
                                                                                                                                                                                                                                                                                                                                 Class: TDNA tagged
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Matches 164; Conservative
                                                    Unpublished
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59

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Query Match

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                                                                                          1 GGTTAAGCGTTTTACTTATGGTTTATATACGAAGGAATATTGCCATTGTTGGAATGC
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                                                 0; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev stage="rosette plants"
/lab_host="DH108"
/clone lib="RAFL"
/note="Site 1" | Site 2: SalI; subjected to cold-treated (1 2, 5, 10, 24 hr)"
131 a 118 c 117 g 117 t 3 others
                                                                                                                                                                                                                                                                                               6:0%, Score 101, DB 9, Length 486,
100.0%, Pred. No. 8.4e-40,
ative 0, Mismatches 0, Indels
         Length 347;
                                                                                                                                                                                                                                                                121 GAAATTGTGTTTATTGCAACAGGTAGAGA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Arabidopsis thaliana"
                             2.8e-64;
                                                                                                                                                                                                                                                                                                                                                                   Contact: Motoaki Seki
Plant Functional Genomics Research Group
         8.9%; Score 149; DB 9;
                    121 GAAATTGTGTTTATTGCAACAGGTAGAGA 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana (thale cress)
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/db_xref="taxon:3702"
/clone="RAFL07-08-P04"
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Matches 149; Conserv
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AV825375
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/mol_type="genomic DNA"
/strain="columbia on"
/db_xref="caxon:3702"
/dlone="SALK_IG0685.39.30.x"
/clone="SALK_IG0685.39.30.x"
/clone="DL="Arabidopais thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
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1 (bases 1 to 347)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thalians: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_srage="two to six-week old"
/clone_lib="Arabidopsis thaliana aboveground organs two to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1588 ACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTCGTCGTCATCT 1647
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Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 ACGCCGTTAAAACGATTCTTTCCCATTGTATCCGCTTTTAACAACTCTCGTCGTCATCTC
                                                                                                                                                                                                                                                                                                                                                                                          1528 TITCCTGCTCCTATATATATATCTGACGAGTCACATTTAGTAATCTCCTTGGACGTGTA
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
                                                                                                                                                                                                                                                                                                      Score 150; DB 29; )
Pred. No. 8.7e-65;
0; Mismatches 0;
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/clone="APZ63b12F"
tissue_type="aboveground organs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Arabidopsis thaliana"
/mol_type="mRNA"
/strain="Columbia"
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AV521636.1 GI:8681163
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Best Local Similarity 100.0
Matches, 150; Conservative
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Figure Functional Galences Center
3-1-1 Koyadai, Tsukuba. Ibaraki 305-0074, Japan
Tel: 81-298-36-4389
Fax: 81-298-36-9060
Email: mseki@rtc.riken.go.jp
An Arabidopsis full-langth cDNA library was constructed essentially as reported previously (Seki et al., 1998).cDNA cleaved with BamHI and XhoI was ligated to modified Lambda FLC-1 vector (Carninci et al., submitted for publication) digested with BamHI and Sali: This clone is in a modified pBluescript vector. Please visit our web eite (http://www.gsc.riken.go.jp/e/plant/index_e.html) for further details.
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Bukaryota Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;

Bukaryota Viridiplantae; Streptophyta, Embryophyta; Tracheophyta;

jernotabhyta; Magnollophyta; eudicotyledons; core endicots; rosids;

l (bases 1 to 486)

Seki,M., Narusaka,M., Ishida,J., Kamiya,A., Satou,M., Nakajima,M.,

Sono,Y., Sakurai,T., Carninci,P., Kamiya,A., Satou,M., Ishii,Y.,

Arakawa,T., Shibata,K., Shinagawa,A., Muramatsu,M., Hayashizaki,Y.

and Shinozaki,K.
241 GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC 182
                                                                                                                                                                                    181 TTTTTCAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 122
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Arabidopsis thaliana (thale cress)
Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplanae; Streptophyta; Embryophyta; Tracheophyta;
Bermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
curosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases II to 146)
Alonso,J.M., Leisse,T.J., Barajas,P., Chen,H., Cheuk,R., Gadrinab,C., Jeske,A., Karnes,M., Kim,C.J., Parker,H., Prednis,L., Shinn,P., Zimerman,J. and Ecker,J.R.
A Sequence-Indexed Library of Insertion Mutations in the Arabidopsis Genome
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Arabidopeis thaliana
Bukaryota, Viridiplantae, Streptophyta; Embryophyta, Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db xref="taxon:3702"
/clone="SALK 038853"
/clone="SALK 038853"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/note="PCR was performed on Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
a 44 c 27 g 42 t
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                                                                                                                                                                                                                                                                                                                                                                      Unpublished
Contact: Joseph R. Ecker
Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Fax: 888 558 658 678
Fax: 888 558 638 640
Fax: ecker@salk.edu
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At294580.
Class. TDNA tagged.
Location/Qualifiers
Location/Qualifiers
/organism="Arabidopsis tha"/mol_type="genomic DNA"/mol_type="genomic DNA"/"--=in="Columbia 0"
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CC459772.1 GI:31343739
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   BH617024.1 GI:18427119
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CC459772/c
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 378)
Mhite,J.a., Todd,J., Newman,T., Focks,N., Girke,T., Martinez de
Mhite,J.a., Todd,J., Newman,T., Focks,N., and Benning,C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: benning@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Zoology Bldg., 1735 Nail Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                               BES23004 arabidopsis developing seed Arabidopsis thaliana cDNA Clone M31B6 5', mRNA sequence.
BES23004.1 GI:9780982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Benning, C
Dept. of Biochemistry & Molecular Biology
Michigan State University
224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBLIO24 146 bp DNA linear GSS 30-JAN-2002 SALK 035853 Arabidopsis thaliana TDNA insertion lines Arabidopsis thaliana genomic clone SALK_035853, genomic survey sequence. BH617024
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Arabidopsis developing seed"
/note="Organ: Developing seed; Vector: pBluescript SK-;
Site_1: EcoR1; Site_2: XhoII"
-97 c 81 g 92 t
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100.0%; Pred. No. 1.2e-31;
tive 0; Mismatches 0; Indels
1637 GICGICATCICCACCGICCGITITICICICAGCIAIATITIA 1677
                                             GIGGICALCICCACCGICITITICICICITITITIA 101
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/dev_stage="5-13 days after flowering"
/lab_host="E.coli"
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/mol_type="mRNA"
strain="Columbia"
/db_xref="raxon:3702"
/clone="M31B6"
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Matches 85; Conservative
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Fax: 517 353 9334
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Matches 26, Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BH493162 825 bp DNA linear GSS 13-DEC-2001
BOGGH91TR BOGO Brassica cleracea genomic clone BOGOH91, genomic
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                                                                                                                                                                                                                                                                                                                                                                                  /clone="SALK 133376.34.05.x"
/clone lib="Arabidopsis thaliana TDNA insertion lines"
/clone lib="Arabidopsis thaliana Innes"
/clone lib="Arabidopsis thaliana lines
each of which contains one or more TDNA insertion
elements. The resultant fragment for each line was
directly sequenced to determine the genomic sequence at
the site of insertion. Details of the protocols used can
be found at http://signal.salk.edu/tdna_protocols.html"
130 c 102 g 166 t 42 others
                                                                                                                                                                                                    This is single pass sequence recovered from the left border of
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Sequence-Indexed Library of Insertion Mutations in the
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DNA is from a doubled haploid provided by Tom Osborn.
Seq primer: TR
Class: sheared ends.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 600;
                                                                Salk Institute Genomic Analysis Laboratory (SIGNAL)
The Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 558 4100.x1752
Erx: 858 558 6379
Email: ecker@salk.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Indels
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2.4%; Score 40; DB 29; L
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 40; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9712 Medical Center Drive, Rockville, MD
Tel: 301-838-3523
Fax: 301-838-0208
                                                                                                                                                                                                                                                                                                      organism="Arabidopsis thaliana"
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/mol_type="genomic DNA"
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                                                                                                                                                                                                                                                                                                                            mol type="genomic DNA"
strain="Columbia 0"
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clone lib="BOGO"
                                                          Contact: Joseph R. Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BH493162.1 GI:17701266
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TIGR
                                                                                                                                                                                                                                           Class: TDNA tagged
                     Arabidopsis Genome
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BH493162
                                    Unpublished
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                                  JOURNAL
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RESULT 11

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FEATURES

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Li, Y., CROSSO, M., Strizhov, N. and Weisshaar, B.

Direct Submission

Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Submitted (17-JUN-2002) Weisshaar B., Max-Planck-Institut fuer
Subchtungsforschung, Carl-von-Linne-Weg 10, Koeln, 50829, Germany
This sequence is recovered from the left border of the T-DNA. It
indicates an insertion within the locus defined by clone F4H6. The
sequences are generated at the MPI for Plant Breeding Research in
the context of the GABI-Kat.project. GABI-Kat is part of the German
Plant Genomics program designated 'GABI'. Information on line
availability can be found at:
http://www.mpiz-koeln.mgg.de/GABI-Kat/.
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/note="PCR was performed on DNA from Arabidopsis thaliana
plants (TI) which were transformed with the T-DNA from
vector pAC16. The lines contain one or more T-DNA
insertions. The DNA fragment(s) resulting from the PCR
were directly sequenced to determine the genomic sequence
flanking the insertion. Sequences displaying significant
similarity to the A. thalaina nuclear genome sequence
processed for submission. T-DNA derived sequences were
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Arabidopsis thaliana T-DNA flanking sequence GK-122806-012551,
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Arabidopsis thaliana
Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids II, Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rosso,M., Strizhov,N., Li,Y., Reiss,B., Dekker,K. and Weisshaar,B. A new Arabidopsis thaliana T-DNA mutagenised population (GABI-Kat) for flanking sequence tag based reverse genetics Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strizhov, N., Li, Y., Rosso, M., Viehoever, P., Dekker, K., Saedler, H. and Weisshaar, B.
                                                                                                                                                                                                                                                                     Gaps
/note="Vector: pHOS1; Site 1: BstXI; 2-3 kb sheared genomic DNA inserted into PHOS1 using BstXI linkers' 174 c 137 g 222 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A pipeline for automated high-throughput generation of F% (flanking sequence tags) from Arabidopsis thaliana T-DNA transformed lines
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                                                                                                                                                                                      1.6%; Score 26; DB 28; Length 825; ilarity 100.0%; Pred. No. 0.15; Conservative 0; Mismatches 0; Indels
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/mol_type="genomic DNA"
/strain="columbia 0"
/doxref="taxon:3702"
/clone="GK-122806-012551"
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                        91 AATGGGGTCCAACCCCAAGTATGGGC 66
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sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/sexipts/gethtml2.pl?tl=&t2=RC4-HT0887-250 800-012-d07&t3=2000-08-25&t4=1) Seq primer: puc 18 forward High quality sequence start: 16 High quality sequence stop: 154. Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="Adult"
/clone lib="HT0887"
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                     Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.P., Coddman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deolliveira, F.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
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Bonaldo,M.F., Lennon,G. and Soares,M.B.
                                                                                                                                                                                                                                                                                                                                                  Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bonaldo,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
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MI-P-E4-abq-h-11-1-UM.s1 MI-P-E4 Sus scrofa cDNA clone
MI-P-E4-abq-h-11-1-UM 3', mRNA sequence.
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                                                                                                                                                                                                                                  sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
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iive 0; Mismatches 0; Indels
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54 c 45 g 39 t
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/mol_type="mRNA"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: +55-11-2704922
Fax: +55-11-2707001
Emal: asimpson@ludwig.org.br
This sequence was derived from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           416 TTATCCCTCTGTGGTGGACCC 436
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   (bases 1 to 178)
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(bases 1 to 162)

Adams, M.D., Rounnsley, S.D., Zhao, S., Field, C.E., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., Shizuya, H., Simon, M. and Venter, J.C.
Simon, M. and Venter, J.C.
Building (1998)
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Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
Seq primer: Ml3 Reverse
Class: BAC ends.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
   Gaps
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/clone_lib="CIT-HSP"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
                                                                                                                                                                                                                                                              AQO55392 11-HSP Homo sapiens genomic clone 2344P6, CIT-HSP-2344P6, TR CIT-HSP Homo sapiens genomic clone 2344P6,
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Contact: Mark Adams
Department of Bukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
   0; Indels
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Pred. No. 50;
Mismatches
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mol_type="genomic DNA"
db_xref="taxon:9606"
clone="2344P6"
                                                           1308 ATTACTAAACAATAAAAGAAAA 1329
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   22; Conservative
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3E933474/c
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Q055392
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Molecular Generics Laboratory, Department of Animal Science
lows State University
2018 Kildee Hall, Ames, IA 50011-3150, USA
2018 Tals: 5122942401
Email: *CKU9918@elastate.edu
The sequence contained an oligo-dT track that was present in the
Cligonuclectide that was used to prime the synthesis of first
stand CDNA and therefore this may represent a bonafide poly. A
tals. The sequence contained any represent a bonafide poly. A
tals. The sequence track served to verify it as a clone from the
non-normalized embryc at gestational day 14 library CDNA Library
Preparation: RW Woods, UA Green, RS Prather 142 Animal Science
Animal Science
Nessarch Counting, 65311 Clone distribution: clones will be
available through Research Genetics (www.resgen.com)
Seq primer: M13 Foward
POLYA-Yes

1.258
Contion/Oualifiers
1.258
Corganism="State and Animal Science"

**Mol type="MRNA"

**Crossbreed"

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Ouery Match 1.3%; Score 21; DB 10; Length 258; Best Local Similarity 100.0%; Pred. No. 51; Matches 21; Conservative 0; Mismatches 0; Indels

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Gaps

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150 TGTGGTTAGTGAAAAGTAAAA 170

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Search completed: February 2, 2004, 05:01:24 Job time : 3888.05 secs

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US-08-891-7893-1
US-08-91-7893-1
US-09-100-391-1
US-09-100-391-1
US-09-620-312D-60
US-09-620-312D-60
US-09-382-25-17
US-09-392-115-17
US-08-481-337A-7
US-08-382-25-17
US-09-39-115-17
US-09-39-115-17
US-09-39-115-17
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100.0%; Pred. No. 27;
ive 0; Mismatches
              S-09-451-501-20
S-09-451-501-26
S-08-891-789B-1
S-08-891-789B-3
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                                                                                                                                                                                                                                                                                            ALIGNMENTS
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MOLECULE TYPE: DNA (genomic)
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Best Local Similarity 100.(
Matches 18; Conservative
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nucleic acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
single
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Sequence 72, Appl
Sequence 68, Appl
Sequence 1, Appl
Sequence 5, Appl
Sequence 2704, Ap
Sequence 1, Appl
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Sequence 2, Appli
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Sequence 71, Appl
Sequence 2588, Ap
Sequence 400, App
Sequence 400, App
Sequence 400, App
Sequence 1630, App
Sequence 1630, App
Sequence 71, Appli
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'GgD2_6/ptodata/2/ina/6B_COMB.seq:*
'GgD2_6/ptodata/2/ina/6B_COMB.seq:*
'GgD2_6/ptodata/2/ina/PcTUS_COMB.seq:*
'GgD2_6/ptodata/2/ina/PcTUS_COMB.seq:*
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(c) 1993 - 2004 Compugen Ltd.
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NAME/KEY: transit_peptide
LOCATION: (79)..(213)
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"UBLICATION INFORMATION:
AUTHORS: Lund, Adrian A.
AUTHORS: Blum, Paul H.
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(329)..(1028)
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LOCATION: (736)..(1028)
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LOCATION: (424)..(693)
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LOCATION: (1)..(1028)
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LOCATION: (79)..(735)
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(1)..(1028)
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                                                                                                                                                                               TYPE: DNA
ORGANISM: Zea mays
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; PAGES: 1097-1110
; DATE: 1998-03-00
US-09-249-180-1
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LOCATION: (1)..
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                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Thomasnow, micrael APPLICANT: Stockinger, Eric APPLICANT: Stockinger, Eric APPLICANT: Jaglo-Ottosen, Kirsten APPLICANT: Jaglo-Ottosen, Kirsten APPLICANT: Jardo, Cal-Zhong TITLE OF INVENTION: Plantel Having Altered Environmental Stress Tolerance FILE REPERENCE: 19117.713 Seq List CURRENT APPLICATION NUMBER: US/09/198,119C CURRENT APPLICATION NUMBER: US 09/706,270 PRIOR PILING DATE: 1998-11-23 PRIOR FILING DATE: 1998-09-04 PRIOR FILING DATE: 1998-09-04 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 PRIOR FILING DATE: 1998-02-03 NUMBER OF SEQ ID NOS: 95
SOFTWARE: Patentin Ver: 2.0
SEQ ID NO 68
SEQ ID NO 68
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APPLICANT: Elthon, Thomas E
APPLICANT: Lund, Adrian A
APPLICANT: Brattramakki, Dinakar
APPLICANT: Bhattramakki, Dinakar
APPLICANT: Rhoads, David M.
TITLE OF INVENTION: Isolation and Characterization of Heat Shock Protein
FILE REFERENCE: UNVNS2819
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1.1%; Score 18; DB 4; Length 877;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 18; Conservative 0; Mismatches 0; Indels
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Best Local Similarity 100.0%; Pred. No. 27,
Matches 18; Conservative 0; Mismatches 0; Indels
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                   FEATURE:
OTHER INFORMATION: boCBF5 gene
IS-09-198-119C-72
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ORGANISM: Brassica oleracea
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ORGANISM: Brassica oleracea
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JS-09-198-119C-68/c
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OTHER INFORMATION: Zea Mays L., Line B73
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ATION: (559)..(828)
SR INFORMATION: Heat Shock Domain
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Patent No. 6562958
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, ORGANISM: Acinetobacter baumannii
US-09-328-352-2704
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US-09-249-180-5
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US-08-545-528D-1
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APPLICANT: Elthon, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Lund, Adrian A
APPLICANT: Bhoads, David M.
APPLICANT: Rhoads, David M.
TITLE OF INVENTIONS ISOJULATION and Characterization of Heat Shock Protein
FILE REPERBNCE: UNYN52819
CURRENT APPLICATION NUMBER: US/09/249,180
EARLIER APPLICATION NUMBER: 60/076/014
EARLIER APPLICATION NUMBER: 60/076/014
                        PPLICANT: CLAMMINIANT CALAMONT APPLICANT SARVA, Daniel
APPLICANT: Jiang, Cal-Zhong
FITLE OF INVENTION: Plant Having Altered Environmental Stress Tolerance
FITLE REFERENCE: 1917,713 Seq List
CURRENT APPLICATION NUMBER: US/09/198,119C
CURRENT FILING DATE: 1998-11-23
CURRENT FILING DATE: US 08/706,270
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SOFTWARE: Created in Patentin Ver. 2.0, Edited in WordPerfect 6.1
SEQ ID NO 5
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PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: US 09/018,233
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR PILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/011,575
PRIOR APPLICATION NUMBER: US 09/017,575
PRIOR APPLICATION NUMBER: US 09/018,227
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100.0%; Pred. No.
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PRIOR APPLICATION NUMBER: US 09/018,227
PRIOR FILING DATE: 1998-02-03
PRIOR APPLICATION NUMBER: US 09/018,234
PRIOR FILING DATE: 1998-02-03
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Sequence 5. Application US/09249180
Patent No. 6268548
GENERAL INFORMATION:
  Kirsten
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SOFTWARE: Patentin Ver. 2.0
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APPLICANT GATY L. Breton et.al.

APPLICANT GATY L. Breton et.al.

APPLICANT GATY L. Breton et.al.

TITLE OF INVENTION: NUCLBIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER

TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS

FILE REPERENCE: GT-0599-037A

CURRENT APPLICATION NUMBER: US/09/328,352

CURRENT FILING DATE: 1999-06-04

NUMBER OF SEQ ID NOS: 8252

SEQ ID NO 2704

LENGTH: 2148
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100.0%; Pred. No. 27;
Length 1163;
                                                                0; Indels
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Sequence 1, Application US/08545528D Patent No. 6537773

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APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING AND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
TITLE OF INVENTION: DAN C.
TITLE OF INVENTION: DAN SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE PEPERENCE: 24366-20007 00
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                 DB 3; Length 4411529;
20;
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95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                            0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1755 Jefferson Davis Highway, Fourth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC COMPATIBLE
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/120,827
FILING DATE: 15-SEP-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                       1.1%; bcc.
100.0%; Pred. No. --
                                                                     CURRENT APPLICATION NUMBER: US/09/103,840A; CURRENT APPLICATION NUMBER: US/09/103,840A; NUMBER: US/09/103,840A; NUMBER: OF SEQ ID NOS: 2; SOFTWARE: Patentin Ver. 2.1; SEQ ID NO 1; SEQ ID NO 1; TENCTH: 4411529; TYPE: DNA
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100.0%; Pred. No.
                                                                                                                                                                                                                                                                     TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OFFINEM: MYCOPACTION: H37Rv
US-09-1103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4154513 CGTCGTCATCTCCACCGT 4154496
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5525495man F.
REGISTRATION NUMBER: 24,618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCACCGT 1653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 71
FELECOMMUNICATION INFORMATION: (703)413-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: RNA (genomic)
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Best Local Similarity 100.
Matches 18; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
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Best Local Similarity
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STREET: 17
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                                                                                 APPLICANT: Fraser et al.

APPLICANT: Fraser et al.

TITLE OF INVENTION: Nucleotide Sequence of the Mycoplasma Genitalium Genome, Fragment
Patent No. 653773

TITLE OF INVENTION: Thereof, and Uses Thereof

TITLE OF INVENTION: Thereof, and Uses Thereof

FILE REFERENCE: P8193P1

CURRENT APPLICATION NUMBER: US/08/545,528D

CURRENT APPLICATION NUMBER: US 08/488,018

PRIOR FILING DATE: 1995-06-07

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 1

SOFTWARE: PatentIn version 3.1

LENGTH: 580073
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COTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WHITE, Owen R. APPLICANT: FRASER, Claire M. APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REPERBNCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 SOFTWARE: PATENTIN VET. 2.1
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23;
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100.0%; Pred. No....
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355690 Arrirgidaaaagaaa 355707

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1332 ATTTTGTGAAAAGAGAAA 1349

TYPE: DNA
ORGANISM: Mycoplasma genitalium
IS-08-545-528D-1

equence 2, Application US/09103840A atent No. 6294328

ESULT 11 JS-09-103-840A-2/c

APPLICANT: FLEISCHMAN, Robert D.

TYPE: DNA ORGANISM: Mycobacterium tuberculosis

SEQ ID NO 2 LENGTH: 4403765

4146706 cercercarcrecacer 4146689

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1636 CGTCGTCATCTCCACCGT 1653

Query Match Best Local Similarity 100. Matches 18; Conservative

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Length 210;

DB 4;

Mismatches

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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR FILING DATE: 1997-08-14
NUMBER: OF SEQ ID NOS: 5674
LENGTH: 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Search completed: February 2, 2004, 07:59:13 Job time : 134.678 secs
                                                                                                                                                                                                                                                                                                                                    Query Match 1.0%; Score 17; Best Local Similarity 100.0%; Pred. No. Matches 17; Conservative 0; Mismatc
                                                                                                                                                                                                                                      ; TYPE: DNA; Caphylococcus epidermidis
US-09-134-001C-2588
                                                                                                                                                                                                                                                                                                                                                                                                                                       221 AAACAAGCATCATTAAA 237
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                                                                                                                                                                                                                                                                             APPLICANT: KEENE, JACK D.
APPLICANT: KING, PETER H.
APPLICANT: LEVINE, TODD
TITLE OF INVENTION: METHODS AND COMPOSITIONS USEFUL IN THE
TITLE OF INVENTION: RECOGNITION, BINDING BAND EXPRESSION OF RIBONUCLEIC ACIDS
TITLE OF INVENTION: INVOLVED IN CELL GROWTH, NEOPLASIA AND IMMUNOREGULATION
NUMBER OF SEQUENCES: 101
  Gaps
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ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESSEE: P.C.
STREET: 1755 Jefferson Davis Highway, Fourth Floor
GITY: Alington
STATE: Virginia
COUNTRY: U.S.A.
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  Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,675
FILING DATE: 07-JUN-1996
CLASSIFICATION: 536
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CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION WUBER: US 08/120,827
FILING DATE: 15-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Oblon, No. 5773246man F.
REGISTRATION WUMBER: 24,618
REFERENCE/DOCKET NUMBER: 714-158-0 CIP
0; Mismatches
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                                                                                                                                                                                                              Sequence 71, Application US/08478675
Patent No. 5773246
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                                               1315 AACAATAAAAGAAAAC 1331
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IBM PC compatible
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy dis
COMPUTER: IBM PC Compat
OPERATING SYSTEM: PC-DO.
SOFTWARE: Patent?
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
  Conservative
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STRANDEDNESS: unkn
                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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  Matches 17;
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ult being printed, ibution.		Description	Sequence 3729, Ap	Sequence 3729, Ap	Sequence 54, Appl	Sequence 707, App	Sequence 1633, Ap	Sequence 306, App		Sequence 54726, A	Sequence 294129,	Sequence 54726, A	Sequence 294129,	Sequence 9987, Ap	Sequence 14103, A	Sequence 18166, A	Sequence 5678, Ap	
score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	SUMMARIES	ΙD	US-09-938-842A-3729	US-09-938-842A-3729	US-09-930-213-54	US-09-803-719-707	US-09-803-719-1633	US-09-930-213-306	US-10-191-807-3	US-10-027-632-54726	US-10-027-632-294129	US-10-027-632-54726	US-10-027-632-294129	US-09-815-242-9987	US-10-029-386-14103	US-10-242-535A-18166	US-09-983-965-5678	
qual sis			101	12	13	11	11	13	12	13	13	4	14	g	13	13	50	
an or e y analy		Query Match Length DB	1677	1677	330	394	407	2000	108359	627	627	627	627	768	199	281	377	
ater th rived b	ьķо	Query Match	100.0	100.0	1.3	1.3	1.3	1.3	1.3	1.2	1.2	1.2	1.2	1.2	1.1	1.1	1.1	
ore gre d is de		Score	1677	1677	21	21	21	21	21	20	20	20	20	20	19	19	19	
B. AT		Result No.	н	73	e	4	ഹ	9	7	ω υ	о О	c 10	0 11	c 12	c 13	c 14	15	

GenCore version 5.1.6  Copyright (c) 1993 - 2004 Compugen Ltd.  OM nucleic - nucleic search, using sw model  Run on: February 2, 2004, 03:00:32; Search time 1254.7 Seconds (without alignments)  Title: Welfect score: 1677  Sequence: 1677  Scoring table: OLIGO NUC  Gapop 60.0, Gapext 60.0  Searched: 2434939 seqs, 182278265 residues  Word size: 0  Total number of hits satisfying chosen parameters: 4869878  Minimum DB seq length: 0	

Sequence 88863, A Sequence 88862, A Sequence 230239, Sequence 230239, Sequence 133067, Sequence 133067, Sequence 2975, Ap Sequence 2975, Ap Sequence 8202, Ap Sequence 8202, Ap Sequence 8202, Ap Sequence 8202, Ap Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262153, Sequence 262154, Sequence 262153, Sequence 262154

Sequence 262153, Sequence 262154, Sequence 122375,

Sequence 122375, Sequence 30495, 2 Sequence 30496, 2 Sequence 30496, 2

Sequence 3833, A Sequence 3833, A Sequence 1592, A

ALIGNMENTS

## Post-processing: Listing first 45 summaries Database

shed Applications NA:*	6/ptodata/1/pubpna/USU/_F 6/ptodata/1/pubpna/PCT_NE	2_6/ptodata/1/pubpna/US06 NEW PUB.	6/ptodata/1/pubpna/US06_PUBCOMB.se	_6/ptodata/1/pubpna/US07_NEW_PUB.s	A/PCTUS PUBCOMB.	A/USO8 NEW PUB.se	n2_6/ptodata/1/pubpna/US08_PUBCOMB.	n2_6/ptodata/1/pubpna/US09A PUBCOMB	gn2_6/ptodata/1/pubpna/US09B	6/ptodata/1/pubpna/US09C	n2_6/ptodata/1,	n2_6/ptodata/1/pubpna/US09_NEW_PUB.s	6/ptodata/1/pubpna/US10A_PUBCOMB.	n2_6/ptodata/1/pubpna/US10B	_6/ptodata/1/pubpna/U	: /cgn2_6/ptodata/1/pubpna/US60_NEW_	6/ptodata/1/pubpna/US60
•••																	

APPLICANT: Harper, Jeff.
APPLICANT: Kreps, Joel
APPLICANT: Wang, Xun
APPLICANT: Wang, Xun
TITLE OF INVENTION: SAME, AND METHODS OF USE
TITLE OF INVENTION: SAME, AND METHODS OF USE

Application US/09938842A

is the number of results predicted by No. Pred.

CURRENT APPLICATION NUMBER: US/09/938/842A CURRENT FILING DATE: 2001-08-24	27,866		PRIOR APPLICATION NUMBER: US 60/264,647	60/300,111	PRIOR FILING DATE: 2001-06-22		, LENGTH: 1677	TYPE: DNA	psis thaliana	US-09-938-842A-3729		Query Match 1677; Score 1677; DB 10; Length 1677;	Best Local Similarity 100.0%; Pred. No. 0;	Matches 1677, Conservative 0; Mismatches 0, Indels 0, Gaps		Qy 1 GGTTAAGCGTTTTACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC.6		Db 1 GGTTAAGCGTTTTACTTATGGTTTATATGCAAGGGAAGAATATTGCCATTGTTGGAATGC		Oy 61 TITTICAGAICAICAAAGGCICCIACAGAITICITAGGGAAIGGITICAGGCITTIGITA 1		Db 61 TTTTTCAGATCATCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 1	
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vUBCOMB.seq:*	y chance to have a	e result being printed,	distribution.			Description		Sequence 3729, Ap	Sequence 3729, Ap	Sequence 54, Appl	Sequence 707, App	Sequence 1633, Ap	Sequence 306, App	Sequence 3, Appli	Sequence 54726, A	Sequence 294129,	Sequence 54726, A	Sequence 294129,	Sequence 9987, Ap	Sequence 14103, A	Seguence 18166, A	Sequence 5678, Ap	
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ATTGTTGGAATGC 60

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121 GAAATTGTGTTTATTGCAACAGGTAGAACATAACCATAGACAGATGTATCTGAAGAGA 180 121 GAAATTGTGTTTTATTGCAACAGGTAGGAACATAACCATAGACAGAC	AAAAACATCGGAATCCAAAACTCAAATTTACCAATCAGCCCAAATTATGATGCTGGGGG TAATGAATGGTATGCTCAATGGTAGGCAAAAGTTGGTGGGGGGGG	481 AAGCCTAAAAGGTTACTACCGGTTTGAATTGGTGTTTAATTCTAATTCC 540 481 AAGCCTAAAAGGTTACTACCGGTTTGACGGTTTTAATTTGGTGTTTAATTCCTAATTCC 540 481 AAGCCTAAAAGGTTACTACCGGTTTGACGGTTTATAATTTGGTGTTTAATTCTAATCCC 540 541 GGATCCGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTGATTTTTGATTTTTGAGG 600 541 GGATCCGTTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTTGAGG 600 601 GGTACCGTTGTTGTTAATCTCAAGGCCACGTTATCGCCAATATTTTGATTTTTGAGTG 600 601 GGTACCGAATGGTGGGGGTCGAATAGTTGGGCCCTCAACAATGTGTGGAACTGAAG 660	601 GGTAGGGATGGAGGTGGATTGGGCCTCACAATGTGGAACTGAAG 660 661 AGAGTAGGGTCCAGGCCCACATTCACATTGCTTTGTAGTGTGGAACTGAAG 660 661 AGAGTAGGGTCCAGGCCCACATTCACATTTTGTTTTTTTT	CCCGAAACAAGTACCAACGAATCAAAATAAGTTTGAATCGGTTACATCTAGTTACGTCGCCCGAACGAA	901 CCGGATTGTACAAGTACATAAGTATGCGTATAGTGTGTGT	ATTAGCTTTTTGGTGGCGCAGCCTTGTGACCTACATTAATGGGGTCCAACCCAAGTATG GGCTTACAGCTTTTTCCATAAATTAAAGTAAATCTTTTTTGCCTAACCCAATAAAATT GGTTTACAGCTTTTTCCATAAAATTAAAGTAAATCTTTTTTGCCTAACCAATAAAAATT GGTTTACAGCTTTTTCCATAAAATTAAAGTAAAATTTTTTTT
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ESS-REGULATED GENES OF PLANTS, TRANSCENIC PLANTS CONTAINING
ME, AND METHODS OF USE
BEE: US/09/938,842A
001-08-24
IUS 60/227,866 ATTITGAAGCTITICTIAGGTIAAAAAACAAGTATATIACTAAACAAT 1320 ATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATATTACTAAAACAAT 1320 TGTGAAAAGAGAATAAAGTTTACTGGACCCCATTGTACAGATGG 1380 TITIGIGAAAAGAAAAAAGITTACIGGACCCCATIGIACAGAIGG 1380 CTGATAGAAGATAGAGCAATGGAAAGTGATTTGTTCACGTGGTACAA 1440 1440 TTAAAGCTCATCGAACACATCAGGACCGTTGATTTTTCCCGCATCAA 1500 TTAAAAGCTCATCGAACACCATCAGACCGTTGATTTTTCCCCGCATCAA 1500 CTATICTCACTIGITITICCTGCTCCTATATATATACCTGACGAGIC 1560 CCTTGGACGTGTAAAACGATTCTTTCCCATTGTATCC 1620 GRATICICACTIGITITICCIGCICCIATATATATATCCIGACGAGTC 1560 TCCTTGGACGTGTAACGCCGTTAAAACGATTCTTTCCCATTGTATCC 1620 CCAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 120 CAAAGGCTCCTACAGATTTCTTAGGGAATGGTTTCAGGCTTTTGTTA 120 NTGCAACAGGTAGAGAACATAACCATAGACAGATGTATCTGAAGAGA 180 PACTIVATGGITTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC 60 PACTTATGGTTTATATGCAACGGAAGAATATTGCCATTGTTGGAATGC 60 CGTCGTCATCTCCACCGTCCGTTTTCTCTCAGCTATATTTTA 1677 TCATTTGGGAGTGTACTAGTAACTAAGTACTAACCAGAATGAGT ACTGATAGAAGATAGAATGGAAAGTGATTTGTTCACGTGGTACAA 100.0%; Score 1677; DB 12; Length 1677; 100.0%; Pred: No. 0; No. 0; Indels 0; Gaps (ve 0; Mismatches 0; Indels 0; Gaps -01-16 R: US 60/300,111 -06-22 379 60/264,647 on US/09938842A 09476A9 haliana 8

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1201   AAAGCTAGGTATTTCATTTGGAGTGTAAAAACAAGTATTACTAAACAT   1320     1261   TTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAACAAGTATTACTAAACAT   1320     1261   TTCTGATTTTGGATTTTGAAGCTTTTCTTAGGTTAAAAAACAAGTATTACTAAACAT   1320     1321   AAAAGAAAAACATTTTGTGAAAAAAAAAAACAAGTATTACTAAACAAT   1320     1321   AAAAGAAAAACATTTTGTGAAAAAAAAAAACATTAACTAGACCCATTGTACAGATGG   1380     1321   AAAAGAAAAACATTTTGTGAAAAAAAAAAAATTAAAGTTTACTAGAACAATG   1340     1321   AAAAGAAAAACATTTTGTGAAAAAAAAAAATTAAAGTTTACTAGAACAATGG   1380     1321   AAAAGAAAAAAATACTGATAGAAAAAAAAATTAAAGTTAAAAATTTGTACAGAAGG   1380     1321   AAAAGATAATAACTGATAGAAAAAAAAATTAAAAGTTATTTGCAGAACAA   1440     1401   TCGGAATGGTTGAATACTCAATGAACAATGGAAAGTGATTTTTTCCAGATCAA   1500     1401   TCGGAATGGTTCTTTAAAGCTCACTCGAACAATCAGAACGAATCAAAAAAAA	TAL  OF DIFFERENTIAL GENE EXPRES  709/930,213 31 0004102.7 , other or unknown , other or unknown	Query Match 1.3%; Score 21; DB 13; Length 330; Best Local Similarity 100.0%; Pred. No. 7.2; Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 416 TTATCCTCTGTGGTGGACC 436
	GGTAGGGATGGGGTGGATAGTTGGGCCTCAACAATGTGTGGAACTGAAG G[	1141 ATTGAAATCTTTCCAACCATAGAAAGTTAAATTTGATCAGCGATGGAATTTTTGTAC 1200

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APPLICANT: ROSENTHAL, ANDRE
APPLICANT: HIXZMANN, BERND
APPLICANT: SCHEMEN, BERND
APPLICANT: SCHEMEN, OCHANES
APPLICANT: SCHEMEN, OCHANES
APPLICANT: TCHE-NITSE, OLEG
APPLICANT: TCHE-NITSE, OLEG
APPLICANT: GRIPS, MARTIN
APPLICANT: SCHNITZ, ANNE-CHANTAL
APPLICANT: SCHNITZ, ANNE-CHANTAL
APPLICANT: SCHNITZ, ANNE-CHANTAL
APPLICANT: SCHES, MARRIN
TILLE REPRESENCE: ABERE-14
CURRENT APPLICATION NUMBER: US/09/930,213
CURRENT FILING DATE: 2001-01-31
NUMBER OF SEQ ID NOS: 885
SOFTWARE: PATCHILIN Ver. 2.1
SEQ ID NO 306
LENGTH: 2000
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                                       Query Match
1.3%; Score 21; DB
Best Local Similarity 100.0%; Pred. No. 7.3
Matches 21; Conservative 0; Mismatches
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Publication No. US20030170625A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            416 TTATCCCTCTGTGGTGGACCC 436
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ORGANISM: Homo sapiens
US-09-930-213-306
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Best Local Similarity
Matches 21, Conserva
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100.0%; Pred. No. 7.3;
cive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kits, David
APPLICANT: Kits, David
APPLICANT: Garcia, Veronica
APPLICANT: Garcia, Veronica
APPLICANT: Stache-Crain, Birgit
TITLE OF INVENTION: Human Genes and Gene Products
FILE REFERENCE: 1644.002
CURRENT APPLICATION NUMBER: US/09/803,719
CURRENT APPLICATION NUMBER: US/09/803,719
PRIOR APPLICATION NUMBER: 60/188,609
PRIOR FILING DATE: 2000-03-09
NUMBER OF SEQ ID NOS: 2396
SOFTWARE: FastSEQ for Windows Version 4.0
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APPLICANT: Bacobedo, Jaime
APPLICANT: Garcia, Michael A.
APPLICANT: Garcia, Pablo Dominiguez
APPLICANT: Studduth-Allinger, Julie
APPLICANT: Reinhard, Christoph
APPLICANT: Giese, Klaus
                                                                                                                                                   Williams, Lewis T.
Escobedo, Jaime
Innis, Michael A.
Garcia, Pablo Dominiguez
Sudduth-Klinger, Julie
Reinhard, Christoph
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Publication No. US20030044783A1
148 TTATCCCTCTGTGGTGGACCC 168
                                                                                           Application US/09803719
5. US20030044783A1
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Crkvenjakov, Radomir
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Randazzo, Filippo
Kennedy, Giulia C.
Pot, David
Kassam, Altaf
Lamson, George
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Kennedy, Giulia C.
Pot, David
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Drmanac, Snezana
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CORGANISM: Homo sapiens
US-09-803-719-707
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Best Local Similarity
Matches 21; Conserv
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Sequence 294129, Application US/10027632
Publication No. US20030204075A9
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) LOCATION: (1)...(627)
COTHER INFORMATION: n = A,T,C or G
US-10-027-632-294129
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Best Local Similarity 100.
Matches 20; Conservative
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ORGANISM: Human
FEATURE:
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TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US 60/18,066
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-07-12
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 2000-03-29
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-11-23
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-10-28
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-09-8
PRIOR FILING DATE: 1999-08-09
NUMBER OF SEQ ID NOS: 325720
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 54726
LENGTH: 627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 1.3%; Score 21; DB 15; Length 108359; Best Local Similarity 100.0%; Pred. No. 13; Matches 21; Conservative 0; Mismatches 0; Indels 0;
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                                                     TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: CL001275-PROV
CURRENT APPLICATION NUMBER: US/10/191,807
CURRENT FILING DATE: 2002-07-10
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
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Sequence 54726, Application US/10027632
Publication No. US20030204075A9
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; OTHER INFORMATION: n = A,T,C or G
JS-10-191-807-3
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OTHER INFORMATION: n = A,T,C or G
JS-10-027-632-54726
                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
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Best Local Similarity
Matches 20; Conserva
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ORGANISM: Human
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ORGANISM: Human
                                                                                                                                                                                                                        SEQ ID NO 3
LENGTH: 108359
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TITLE OF INVENTION:

APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide

TITLE OF INVENTION: Polymorphisms in the Human Genome

FILE REFERENCE: 108827.129

CURRENT FILING DATE: 2002-04-30

PRIOR PILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR PILING DATE: 2000-04-24

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-03-29

PRIOR FILING DATE: 1999-11-28

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PRIOR FILING DATE: 1999-10-28

PRIOR FILING DATE: 1999-09-28

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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Oldentification and Mapping of Single Nucleotide
TITLE OF INVENTION: Oldentification and Mapping of Single Nucleotide
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/00/12 0.000
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/195,218
PRIOR PILING DATE: 1090-03-24
PRIOR PILING DATE: 1099-11-23
PRIOR PILING DATE: 1999-11-23
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR PILING DATE: 1999-09-28
PRIOR PILING DATE: 1999-09-28
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25;
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100.0%; Pred. No. ...
0; Mismatches
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R OF SEQ ID NOS: 325720
ARE: FastSEQ for Windows Version 4.0
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Dolymorphisms in the Human Genome
FILE REFERENCE: 108827.129
CURRENT APPLICATION NUMBER: US/10/027,632
CURRENT APPLICATION NUMBER: US/02-04.30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR APPLICATION NUMBER: US 60/198,676
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/193,483
PRIOR PILING DATE: 2000-04-20
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR PILING DATE: 1999-10-24
PRIOR APPLICATION NUMBER: US 60/157,363
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 294129
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GENERAL INFORMATION:
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320020061569A1
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; OTHER INFORMATION: n = A,T,C or G
US-10-027-632-294129
                                                                                                                        = A,T,C or G
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1.2%; Scc
Best Local Similarity 100.0%; Pr
Matches 20; Conservative 0;
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Best Local Similarity 100.0%; P
Matches 20; Conservative 0;
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Trawick, John D.
                                                             NAME/KEY: misc_feature
                                                                                         LOCATION: (1) ... (627)
CTHER INFORMATION: n
US-10-027-632-54726
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ORGANISM: Human
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Sequence 14103, Application US/10029386
Publication No. US20030194704A1
GENERAL INFORMATION:
APPLICANT: Pen, David R.
APPLICANT: Rank, David R.
APPLICANT: Hank, David R.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR GITTLE OF INVENTION: EXPRESSION ANALYSIS TWO
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
CURRENT APPLICATION NUMBER: US/10/029,386
CURRENT FILING DATE: 2001-12-20
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(: EXPRESED IN HEART, SIGNAL = 1.6
I: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
V: EXPRESSED IN BRAIN, SIGNAL = 1.8
V: EXPRESSED IN HELA, SIGNAL = 1.1
N: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
N: EXPRESSED IN LUNG, SIGNAL = 1.2
N: EXPRESSED IN LUNG, SIGNAL = 1.2
N: EXPRESSED IN LUNG, SIGNAL = 1.2
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APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT PILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-05-23
PRIOR FILING DATE: 2000-05-24
PRIOR PILING DATE: 2000-05-24
PRIOR PELICATION NUMBER: 60/207,727
PRIOR PELICATION NUMBER: 60/245,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2000-12-22
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastERQ for Windows Version 4.0
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Pred. No. 26;
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SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 14103
LENGTH: 199
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ORGANISM: Salmonella typhi
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              , NAME/KEY: CDS
; LOCATION: (1)...(768)
US-09-815-242-9987
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Best Local Similarity
Matches 20; Conserv
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Sequence 5669, Application US/09983965
Fatent No. US20020137160A1
GENERAL INFORMATION:
APPLICANT: Warren, Wesley C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Byatt, John C.
APPLICANT: Machialgan, Nagappan
TITLE OF INVENTION: MUSCIE AND FAT DEPOSITION
TITLE OF INVENTION: MUSCIE AND FAT DEPOSITION
TITLE OF INVENTION: WUSCIE AND FAT DEPOSITION
FILE REPRENCE: 37-21 (10297) C
CURRENT FILING DATE: 2001-10-26
FRIOR APPLICATION NUMBER: US 09/465,231
FRIOR APPLICATION NUMBER: US 60/113,678
FRIOR APPLICATION NUMBER: US 60/113,678
FRIOR FILING DATE: 1998-12-15
FRIOR FILING DATE: 1998-12-17
FRIOR FILING DATE: 1998-12-17
FRIOR FILING DATE: 1998-12-17
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APPLICANTON: Compositions and Methods Relating to Osteoarthritis
FILE REPRENCE: 4231/2005
CURRENT APPLICATION NUMBER: US, 10/042,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR PILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-07-13
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-12
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: Patentin version 3.2
SEQ ID NO 18166
LENGTH: NA
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Length 199;
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                                                   0; Indels
DB 13;
73;
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100.0%; Pred. No. ...
                                                   Mismatches
Score 19;
Pred. No.
                                                                                                                                                                                                                                                                           Sequence 18166, Application US/10242535A bublication No. US20040013663A1 GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | NAME/KEY: misc_feature
| LOCATION: (31)...(31)
| OTHER INFORMATION: n is a, c, g, or
| US-10-242-535A-18166
                                                                                                 1259 GTTTCTGATTTTGGATTTT 1277
Query Match
1.1%; Soc
Best Local Similarity 100.0%; Pr
Matches 19; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.0
Matches 19; Conservative
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